From:

Shukla, Ram

Sent:

Tuesday, April 20, 2004 4:41 PM

To:

STIC-Biotech/ChemLib

Subject:

10/055,106

Please provide sequence search for:

SEQ ID NO 1 Nucleic acid encoding SEQ ID NO 2 12mer Oligosearch

Thanks.

Ram R. Shukla, Ph.D. Primary Examiner AU 1632 2D29 Remsen Bldg Mailbox 2C18

Phone: (571) 272-0735 Fax: (571) 273-0735

APR 20 20

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Searcher: \_\_\_\_\_\_Phone: \_\_\_\_\_\_\_
Location: \_\_\_\_\_\_
Date Picked Up: \_\_\_\_\_\_/
Date Completed: \_\_\_\_\_/
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TYPE OF SEARCH:

NA Sequences:

AA Sequences:

Structures:

Bibliographic:

Litigation:

Full text:

Patent Family:

Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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PhevalileAlavalalavalileLeuLeuvalPheGlnValPheileIleMetLeuMet 207
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CTCTATGTCCTCATAAAAACCTATCACAAGAAGTCAGCCTTCCAAGTATACATGATTAAT 421
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242 GGAAATCTGACAGTATCTTCTGCCACATGCCATGACACTATGATGACTTCCGCAATCAA 301
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Matches:
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; SEQ 1D NO 7
; LENGTH: 1358
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (230)...(1243)
US-10-400-991-7
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Best Local Similarity:
Query Match:
DB:
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995	267	. 1055	284	1115	
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Search completed: April 25, 2004, 22:24:44 Job time : 488 secs

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APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Mile Mile S.
APPLICANT: Mile Mile S.
APPLICANT: Weich, Nadine S.
APPLICANT: Weich, Nadine S.
APPLICANT: White, David J.
APPLICANT: Masserh. Kyle J.
APPLICANT: Masserh. Kyle J.
APPLICANT: Masserh. Kyle J.
APPLICANT: Masserh. Kyle J.
APPLICANT: Williamson, Mark J.
APPLICANT: Chun, Miyoung S.
TITLE OF INVENTION: 39404, 31231, 26904, 31231, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 18037, 
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706 AIGGICGIGACCGCTGTTTTTAGTCAGTTTCATGCCATATTCAACGTACCATT 765
                                 208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn 227
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   171 LysGlu---LeuAlaTyrThrTyrValLysIleIleAsnTyr-----MetIleValIle 187
                                                                                                            188 PheValileAlaValAlaValIleLeuLeuValPheGlnValPheIleIleMetLeuMet 207
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NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Membelogical Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Heam-tological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692 or 58874
FILE REFERENCE: MPI2001-288P1(M)
FULE REFERENCE: MPI2001-288P1(M)
CURRENT FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
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313 GTCAACCTCTATTGTAGCATCTTCTTATGACAGCC------ATGAGC 354
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13 GGAAATCTGACAGTATCTTCTGCCACATGCCATGACACTATTGATGACTTCCGCAATCAA 72
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Conservative:
Mismatches:
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Matches:
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US-10-290-078-20
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ORGANISM: Homo Sapien
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LENGIH: 1014
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TACAATGAGCAACAGTGCTTTAGATTCCATAAAGAACTTGGCCATGATTCTGTGCGAGTT
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Matches:
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      TYPE: DNA ORGANISM: Mus musculus
                                                                  Percent Similarity:
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US-09-782-974C-21/c
                                         Alignment Scores:
Pred. No.:
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LENGTH: 810
                  , ORGANISM: M
US-10-366-504-1
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Sequence 21, Application US/09782974C
Publication No. US20030082534A1
APPLICANT: Vogeli, Gabriel
APPLICANT: Vogeli, Gabriel
APPLICANT: Parodi, Lind, Peter Ind., P
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APPLICANT: Dressler, Holly
APPLICANT: Dressler, Holly
APPLICANT: Cai, Jidong
APPLICANT: Wright, Paul
TITLE OF INTENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND I
TITLE OF INTENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND I
TITLE OF INTENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND I
TITLE OF ILLING DATE: 2003-02-13
FRICAR APPLICATION NUMBER: US 60/356,686
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN Version 3.0
SEQ ID NO 1
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US-10-366-504-1
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                               ValPheileileMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu
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Sequence 1, Application US/10085233B
Sequence 1, Application No. US20030087249A1
GENERAL INFORMATION:
TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
FILE REFERENCE: MPIZOOL-021PIRCPIM
CURRENT APPLICATION NUMBER: US/10/085,233B
PRIOR APPLICATION NUMBER: 60/272,677
PRIOR APPLICATION NUMBER: 60/272,677
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1684
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-085-233B-1
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CRGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (1)...(939)
US-10-085-233B-3
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                   US-10-055-106C-2 (1-305) x US-10-292-798-1007 (1-113306)
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Sequence 3, Application US/10085233B
Publication No. US20030087249A1
GENERAL INFORMATION:
JENERAL INFORMATION:
JITLE OF INVENTION: 93970, A HUMAN G-EROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR AND USES THEREFOR
FILE REFERENCE: MP1201-021PRCP1M
CURRENT RILING DATE: 2002-02-28
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASISEQ FOR WINGOWS VERSION 4.0
SEQ ID NO. 3
SEQ ID NO. 3
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SCHOOL 1007, Application US/10292798

| Publication No. US2003025833A1 |
| GENERAL INFORMATION: |
| APPLICANT: SUMA, MAKINO |
| APPLICANT: ARMAY MAKINO |
| TILE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS |
| TILE REFERENCE: 084335/16 |
| CURRENT FILING DATE: 2002-1.13 |
| PRIOR APPLICATION NUMBER: UP 2001-246789 |
| PRIOR APPLICATION NUMBER: UP 2001-06-18 |
| PRIOR PILING DATE: 2001-06-18 |
| PRIOR PILING DATE: 2010-06-18 |
| SOFTWARE: PATENTIN VET: 2.1 |
| SEQ ID NO 1007 |
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| TENTH: AMBOR OF EMPTION 
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; LOCATION: (98732)..(98784)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112891)..(113106)
US-10-292-798-1007
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ORGANISM: Homo sapiens
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US-10-292-798-1007
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PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/714,449
PRIOR APPLICATION NUMBER: 09/714,449
PRIOR PLLING DATE: 2000-16-16
PRIOR PAPLICATION NUMBER: 60/166,071
PRIOR PELING DATE: 1999-11-19
PRIOR PELING DATE: 1999-11-19
PRIOR PELING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR APPLICATION NUMBER: 60/143,396
PRIOR PELING DATE: 1999-11-28
PRIOR PELING DATE: 1999-12-28
PRIOR PELING DATE: 2000-02-28
PRIOR PELING DATE: 2000-02-28
PRIOR PELING DATE: 2000-02-28
PRIOR PELING DATE: 2000-02-28
PRIOR PELING DATE: 2000-03-28
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PRIOR PELING DATE: 2000-03-31
PRIOR PELING DATE: 2525
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; ORGANISM: Homo sapiens
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921 TACCAGTICTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
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US-09-782-974C-81
US-09-782-974C-81
Sequence 81, Application US/09782974C
Publication No. US20030082534A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Unda Nodo, Linda S.
APPLICANT: Wood, Linda S.
APPLICANT: Wood, Linda S.
APPLICANT: Wood, Linda S.
APPLICANT: Wood, Linds A.
APPLICANT: Wood, Linds A.
APPLICANT: Wood, Linds A.
APPLICANT: WOOD IN NOWER S.
CURRENT PAPLICATION NOWER: US/09/782,974C
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/165,838
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; Sequence 1193, Application US/10017161
; Publication NO. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAXIKO
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ARUTANA, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR FILING DATE: 2001-06-18
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1193
; LENGTH: 1318
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; LOCATION: (201)..(1118)
US-10-017-161-1193
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ORGANISM: Homo sapiens
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LOCATION: (1)..(1318)
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US-10-293-171-1
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            , OTHER INFORMATION: human TGR343
US-10-188-405-9
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100.00%
ORGANISM: Homo sapiens
                                                      Percent Similarity:
Best Local Similarity:
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Sequence 1, Application US/10293171
Publication No. US20030138418A1
APPLICANT: Cai, Jidong
APPLICANT: ANOUNT NUMBER: USAU201/0158 US NP
CURRENT APPLICATION NUMBER: US60/354,150
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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US-10-188405-9
US-10-188405-9
Sequence 9, Application US/10188405
Publication No. US20030082585A1
Publicant No. US20030082585A1
APPLICANT: Tian, Hui
APPLICANT: Dai, Kang
APPLICANT: Cano, Jin-Long
APPLICANT: No. US20030082585A1e1
APPLICANT: APPLICATION NUMBER: US/10/188,405
CURRENT FILING DATE: 2002-07-01
FRIOR FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 9
LENGTH: 918
TYPE: DNA
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publication No. US20030017536A1
general information:
APPLICANT: Pfizer Inc.
APPLICANT: Harland, Lee
TILE REFERENCE: PC10970ACLK
CURRENT APPLICATION: NOWEL POLYPEPTIDE
CURRENT APPLICATION NUMBER: US/10/055,106C
CURRENT FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: GB0010739.1
PRIOR PILING DATE: 2001-01-23
PRIOR PILING DATE: 2001-01-01
SPIOR PPLICATION NUMBER: US 60/267,341
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Version 3.1
SEQ ID NO 1
LENGTH; 918
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Matches:
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Mismatches:
Indels:
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Sequence 2, Application US/10297908A

Publication No. US20040029793A1

GENERAL INFORMATION:

APPLICANT: NO. Takahashi

APPLICANT: HTO, Takahashi

APPLICANT: HTO, Takahashi

APPLICANT: HTO, Takahashi

APPLICANT: HTO, Takahashi

APPLICANT: HTAMAINA, No. US20040029793Aluyuki

APPLICANT: MIYAJIMA, No. US20040029793Aluquki

APPLICANT: MIYAJIMA, No. US20040029793Aluquki

TILE OF INVENTION: No. US20040029793Aluquki

FILE REFERENCE: 2737 USOP

CURRENT APPLICATION NUMBER: US/10/297, 908A

CURRENT FILING DATE: 2001-06-12-11

PRIOR FILING DATE: 2000-16-14

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 2

LENGTH: 918

TYPE: DNA

TYPE: DNA
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                                                                                                                                                                 241 TyrGlnPhePheArglleTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer 260
                                                                                                                                                                                                                                                           721 TACCAGTICTITAGGATCTATTACTTGATGTGACGCATTCCAATGCCTGTAACAGC 780
                                                                                                                                                                                                                                                                                                                                                               781 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG 840
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                             ValPheileileMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu 220
                                                                                                                              PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro 240
                                                               601 GTCTTCATCATTATGTTGATGGTGCAGAAGCTACGCCCACTCTTTACTATCCACCACCAGAG
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; ORGANISM: Homo
US-09-995-225-3
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Matches:
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PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-04-60
PRIOR FILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,326
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-05-06
PRIOR APPLICATION NUMBER: 60/292,356
PRIOR PILING DATE: 2001-05-14
PRIOR PILING DATE: 2001-05-14
PRIOR PILING DATE: 2001-07-31
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TYPE: DNA

; ORGANISM: Homo sapiens

US-09-995-225-3
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Best Local Similarity:
Query Match:
DB:
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Sequence 3, Application US/0999525

Sequence 3, Application US/0999525

Publication No. US2020193584A1

GENERAL INFORMATION:

APPLICANT: Chu, Zhi Liang

APPLICANT: Chu, Zhi Liang

APPLICANT: Chu, Zhi Liang

APPLICANT: Lang, Huong T.

APPLICANT: ARE Cameron

TITLE OF INVENTION: Receptors

FILE REFERENCE: AREN-0308

CURRENT APPLICATION NUMBER: US/09/995,225

CURRENT APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

PRIOR PLING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 60/253,404

PRIOR APPLICATION NUMBER: 60/255,366

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 413, App
Sequence 113, App
Sequence 1038, App
Sequence 1038, App
Sequence 627, App
Sequence 627, App
Sequence 627, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 11, App
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 17, Appli
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Sequence 21, Appl
Sequence 20, Appl
Sequence 7, Appli
Sequence 4, Appli
Sequence 19, Appl
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Sequence 6, Appli
Sequence 1, Appli
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Sequence 3
Sequence 5
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Sequence 3
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US-10-225-567A-417
US-10-225-567A-417
US-10-225-027-1038
US-10-101-510-38
US-10-101-510-38
US-10-101-510-633
US-10-101-510-633
US-10-101-510-633
US-09-744-783-2
US-09-744-783-2
US-09-10-172-21
US-09-914-172-21
US-09-914-122-21
US-09-914-128-2
US-09-914-128-2
US-09-914-1018-2
         US-09-991-225-29
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US-09-866-230-6
US-09-828-478-1
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-MODEL=frame+ p2n.model -bEV=xlh
-OCGR02 1/04/10 - MODEL=frame+ p2n.model -bEV=xlh
-O=(CGR02 1/04/10 - MODEL-frame+ p2n.model -bEV=xlh
-O=(CGR02 1/04/10 - MODEL-frame+ p2n.model -bEV=xlh
-OEGR02 1/04/10 - MODEL-frame+ p2n.model -bEV=xlh
-DB=Published Applications NA -OFMT=fastap -SUPFIX=p2n.mpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRAT=1 - END=-1 - MARTX-ABlosum62
-TRAMS=human40 -cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX-100
-TRAMS=human40 -cdi -LIST=45 - DOCALIGN=200 -TR SCORE=pct -THR MAX-100
-TRAMS=ND=0 - NOTER=LOCAL - OOTMPHT=pto -NORM=ext - HEAPSIZE=S00 -MINLEN=0
-MAXIEN=200000000 -USER=S10055106 @CGN 1 1 221 @runat 2104204 id1132_26226
-NCPUG= -ICPUG=3 -NO_MMAP -LARGEQUERY -NGG SCORES=0 - WAIT - DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 - XGAPOP=10 - XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 - YGAPEXT=0.5 -DELOPE6 - DELOEXT=7
                                                                                                                                April 25, 2004, 19:58:35; Search time 469 Seconds (without alignments) 2932.049 Million cell updates/sec
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1 MPGHNTSRNSSCDPIVTPHL......GGSHWFKQKIIGLMNCVLCR 305
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| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_BW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                            - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2907579 segs, 2254313464 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 2000000000
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Score Match Length DB
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Database :

Result No.

0; Gaps Query Match

3.1%; Score 28; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 28; Conservative 0; Mismatches 0; Indels

0

419 GGACGCTGGTGATTGTCATTGTGGTACC 446

рp ò

Search completed: April 25, 2004, 20:06:18 Job time : 462 secs

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APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0308
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FEATURE:
OCHHER INFORMATION: No. US20020193584Alel Sequence
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence FEATURE: ORGANISM: ORGANISM: OTHER INFORMATION: No. US20030139588A9el Sequence US-09-995-225-26
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Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 29; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: 99/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/25,366
PRIOR PELICATION NUMBER: 60/270,286
PRIOR PELING DATE: 2001-02-20
PRIOR PELICATION NUMBER: 60/28,365
PRIOR PELING DATE: 2001-04-06
PRIOR PELICATION NUMBER: 60/28,365
PRIOR PILING DATE: 2001-04-06
PRIOR PELING DATE: 2001-04-06
PRIOR PILING DATE: 2001-03-03
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CURRENT FILING DATE: 2001-11-26
                                                                 PRIOR APPLICATION NUMBER. 2014-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR PLING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 29
LENGTH: 29
APPLICATION NUMBER: 60/282,356
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5. US20020193584A1
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GENERAL INCRMATION:

APPLICANT Chan, Fair Liang
APPLICANT Chu, Jain Liang
APPLICANT Chu, Jain Liang
APPLICANT Chu, Jain Liang
APPLICANT Dang, Huong T.
APPLICANT Pride, Cameron
TITLE OF INVENTION Endogenous And No. US20030139588A9-Endogenous Versions of Human G
TITLE OF INVENTION Endogenous Logology
TITLE OF INVENTION Receptors
FILE REPRENCE: AREN 0308
CURRENT PAPLICATION NUMBER: US/09/995,225
CURRENT PAPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: PC7/1899/23938
PRIOR PLING DATE: 1998-10-13
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-12
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
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US-09-995-225-26
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            PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR PELING DATE: 2000-12-12
PRIOR PILING DATE: 2001-22-20
PRIOR PILING DATE: 2001-04-66
PRIOR APPLICATION NUMBER: 60/202,365
PRIOR APPLICATION NUMBER: 60/202,266
PRIOR APPLICATION NUMBER: 60/202,266
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-07-14
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Publication No. US20030139588A9
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 29
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ORGANISM: Artificial Sequence
FEATURE:
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Sequence 26, Application US/09995225

Publication No. US20020193584A1

GENERAL INFORMATION:

APPLICANT: Chu, Zhi Liang

APPLICANT: Chu, Zhi Liang

APPLICANT: Dang, Huong T.

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

CURRENT APPLICATION NUMBER: US/09/995,225

CURRENT APPLICATION NUMBER: US/09/995,225

CURRENT APPLICATION NUMBER: US/09/995,225

CURRENT APPLICATION NUMBER: US/09/995,225

FRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1998-10-13
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PRIOR FILING DATE: 2000-11-16
PRIOR PELICATION NUMBER: 60/199,568
PRIOR APPLICATION NUMBER: 60/166,071
PRIOR FILING DATE: 1999-11-17
PRIOR FILING DATE: 1999-11-17
PRIOR PELING DATE: 1999-11-17
PRIOR PELING DATE: 1999-11-19
PRIOR PELING DATE: 1999-11-19
PRIOR PELING DATE: 1999-12-28
PRIOR PELING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 2000-02-28
PRIOR PELING DATE: 2000-03-02
PRIOR PELING DATE: 2000-03-03
PRIOR PELING DAT
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ORGANISM: Homo sapiens
US-09-782-974C-21
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US-09-995-225-26/c
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             CTCCTGGTGAAATGAACACCCGGTCAGTGACCATGGCGGTCATTAACTTGGTGGTG 180
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US-00-782-974C-21/C
; Sequence 21, Application US/09782974C
; Publication No. US20030082534A1
; GARERAL INFORMATION.
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wodeli, Did, Peter
; APPLICANT: Parodi, Linia A.
; TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
; TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
; TITLE OF INVENTION: NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR PAPLICATION NUMBER: 60/165,838
; PRIOR APPLICATION NUMBER: 09/714,449
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		US-10-085-233B-3  US-10-085-233B-3  Sequence 3, Application US/10085233B  Publication No. US20030087249A1  GENERAL INFORMATION:  APPLICATY: GLUCKSMANN, MARIA ALEXANDRA  TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED  TITLE OF INVENTION: RECEPTOR AND USES THEREFOR  FILE REPERENCE: MPLOOI-021PLRCPLM  CURRENT APPLICATION NUMBER: US/10/085,233B  CURRENT APPLICATION NUMBER: 0S/272,677  PRIOR APPLICATION NUMBER: 0S/272,677  PRIOR PRIOR DATE: 2001-03-01  NUMBER OF SEQ ID NOS: 6  SOFTWARE: FaetSEQ for Windows Version 4.0  SEQ ID NO 3  LENGTH: 939  TYPE: DNA  REATURE:  NAME/KEY: CDS  NAME/KEY: CDS  US-10-085-233B-3  US-10-085-233B-3	Query Match         94.1%;         Score 864;         DB 15;         Length 939;           Best Local Similarity         99.9%;         Pred. No. 0;         0;         daps         0;           Matches 914;         Conservative         0;         Mismatches         1;         Indels         0;         Gaps         0;           Qy         1 ATGCCTGGCCACATACTCCAGGATTCCTTCTCGGATCCTATAGTGACACCCCACTTA         84           Qy         61 ATCAGCCTCACTACTACTAGTGCTTATTGGCGGGCTGGTGGTGATTCCATTCTTTC         120           Qy         61 ATCAGCCTCACTACTTCATAGTGCTTATTGGCGGGCTGGTGGTGTCATTTCCATTCTTTTC         120           Db         85 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGTTATTTCCATTCTTTTC         140
Db   12260 TACCAGTTCTTTAGGATCTTTATATGTGTGACGCATTCCAATGCCTGTAACAGC 12319   Qy	RESULT 10 US-10-085-233B-1 Sequence 1. Application US/10085233B Publication No. US20030087249A1 Publication No. US20030087249A1 Publication No. US20030087249A1 TITLE OF INVENTION: MARIA ALEXANDRA TITLE OF INVENTION: RECEPTOR AND USES THEREFOR TITLE REFERENCE: MPI2001-021P1RCP1M CURRENT FILING DATE: 2002-02-28 FRIOR FILING DATE: 2002-02-28 PRIOR FILING DATE: 2001-03-01 NUMBER OF SEQ 1D NOS: 6 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: Home sapiens FEATURE: NAME/KEY: CDS NAME/KEY: CDS COCATURE: NAME/KEY: CDS	atch  1338-1  atch  2338-1  atch  23.10-1  34.4%; Score 867; DB  24.10-1  20.20-20-20-20-20-20-20-20-20-20-20-20-20-2	Oy 241 TGGAIGTTTGGGCCCTTCTGCAAATTGTGAGTGCCATGCTACCACATGTAC 300  411 TGGAIGTTTGGCCTTCTTCTACAAATTTGTGAGTGCCATGCTCCACATGTAC 300  411 TGGAIGTTTGGCCTTCTTCTACAAATTTGTGAGTGCCATGCTGCACATCACTTCA 700  Oy 301 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACATCATCTTCTTCAAGTGC 360  Db 471 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACATCTTCTTCTTCAAGTGC 530  Oy 361 AAAGACAAAGTGCAATTCTACAAAAACTGCATGCTGGCTG

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                                     | MAMEKEY: CDS | MAMEKEY: CDS | MAMEKEY: CDS | LOCATION: (201)...(207) | FEATURE: COSTION: (201)...(207) | FEATURE: COSTION: (11526)...(12452) | FEATURE: COSTION: (37954)...(38097) | FEATURE: COSTION: (37954)...(38097) | FEATURE: COSTION: (39732)...(98784) | FEATURE: COSTION: (39732)...(98784) | FEATURE: MAMEKEY: COSTION: (39732)...(98784) | FEATURE: MAMEKEY: COSTION: (11291)...(113106) | US-10-292-798-1007
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ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
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ORGANISM: Homo sapiens
US-09-782-974C-81
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Best Local Similarity
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1193
LENGTH: 1318
                                                                                                   NAME/KEY: CDS
; LOCATION: (201)..(1118)
US-10-017-161-1193
                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                           FEATURE:
NAME/KEY: source
LOCATION: (1)..(1318)
FEATURE:
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Fublication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ARIN, KIYOSHI
APPLICANT: ARINAM, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
ITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT APPLICATION NUMBER: US/10/246789
PRIOR FILING DATE: 2001-06-18
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Sequence 1, Application US/10293171

GENERAL INFORMATION:
APPLICANT: Eishingdrelo, Haifeng
APPLICANT: Eishingdrelo, Haifeng
APPLICANT: Gassenhuber, Johann

TITLE OF INVENTYON: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND USES 7

FILE REPRENCE: USAV2001/0158 US NP

CURRENT APPLICATION NUMBER: US/01/293,171

CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: US60/354,150

PRIOR FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

FEQUENCE: APPLICATION NOS: 9

SEQ ID NO 1.
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, ORGANISM: homo sapiens
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CRGANISM: Homo sapiens
FRATURE:
CTHER INFORMATION: human TGR343
US-10-188-405-9
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Best Local Similarity 100.
Matches 918; Conservative
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                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 918; DB 13; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels 0
 Sequence 1, Application US/10055106C
Publication No. US20030017536A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Parland, Lee
FILE REPERENCE: PC10970AGLK
CURRENT PILING: PC10970AGLK
CURRENT FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: GB0101739.1
PRIOR FILING DATE: 2001-02-08
NUMBER: OF SEQ ID NOS: 3
NUMBER: PRIOR FILING DATE: 2001-02-08
NUMBER: PRIOR FILING DATE: 2001-02-08
SEQ ID NOS: 3
SEQ ID NOS: 3
                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-10-055-106C-1
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908A-2 tch 100.0%;	Best Local Similarity 100.0%; Fred. No. 0; Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0  Qy 1 ATGCCTGGGCACAATACCTCCAGGAATTCCTCTTGGGATCCTATAGTGACACCCCACTTA 60	т ,		121 CTCCTGGTGAAATGAACACCCGGTCAGTGACCACCATGGCGGTCATTAACTTGGTGGTG 181 GTCCACAGGGTTTTTCTGGTGACAGGCCATTGGCGGTGACGACGAAGACT	181	301	Db. 301 CTCACGTTCTATGTGTGATCTCTGGTCACCGAGATCTCTTCAAGTGC 300 CTCACGTTCTACAAAACTGCAAAAACTGCATGCTGCTGCTGCTGCCAGTGCTGCCAGTGCTGCCAGTGCTGCAATGTGGCATGTGGCAATGTGGCAAAAACTGCATGCTGCTGCTGCCAGTGCTGCCAAGTGCTGCAATGTGGCAATGTGGCAATGTGG	Db 361 AAAGACAAAGTATTCTACAGAAACTGCATGCTGGCTGCCAGTGCTGGCTTGTGTTGTGGGGGGGG	Db 421 AGGTGGTGGTGTTTTAAATTTCAGAAAGAGGTTGGTTAGAAAATTCAGAAAAGAGAGTTGGTTTAAAATTTCAGAAAAGAGGTTGGTT	Db 481 TACAATGAGGAGCACTGTTTTAATTTCACAAAGAGCTTGCTT	541 ATCAACTATATGATGATTTTTTTTTTTTTTTTTTTTTTT	DD 601 GICTTCATCATTATGTTGATGGTGCAGAAGCTACGCCACTCTTACTACTATCCCACCAGAG 660  Qy 661 TTCTGGGCTCAGCTGAAAACCTATTTTTATAGGGGTCATCCTTGTTTGT	Qy 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC 780 Db 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC 780		Qy         841         CTTCTTTGTCTTTGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT         900           Db         841         CTTCTCTTTGTCTTTGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT         900	Oy 901 TGTGTTTTGTGCGTTAG 918	RESULT 4 US-10-055-106C-1
Qy 241 TGGATGTTTGGGCTGCCCTTCTGCAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300	Qy 301 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC 360 Db 301 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC 360	361 AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGTGGCTGCCAGTGCT	351 AAAGACAAAGIGGAAIICIACAGAAACIGCAIGGGIGGCGGCGCGCGC	STGAAAATC	541 ATCAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG 541 ATCAACTATATGATCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTTCCAG 541 ATCAACTATATAGTCTATTTTTCCATAGCTGTTGGTTGTTTTTCCAG	601 GICTICATCATTATGTIGATGGAGAAGGCTACGCCACTCTTTACTATCCCACCAGGAG [	Oy 661 TICTGGGCTCAGCTGAAAACCTATTTTTATAGGGGTCATCCTTGTTTGT	Oy 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCTGTAACAGC 780  Db 721 TACCAGTTCTTTAGGATCTATTACTTGATGTTGTGACGCATTCCAATGCCTGTAACAGC 780	Qy 781 AAGGTIGCATITTATAACGAAATCTICTTGAGTGTAACAGCAATTAGCTGCTATGATTTG 840 Db 781 AAGGTIGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG 840	Oy 841 CTTCTCTTTGTCTTTGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 900  B41 CTTCTCTTTGTGTTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 900	Qy 901 TGTGTTTTGTCCCGTTAG 918 	RESULT 3 US-10-297-908A-2 ; Sequence 2, Application US/10297908A ; Publication No. US20040029793A1	, GENERAL INFORMATION: , APPLICANT: MORIYA, Takeo , APPLICANT: ITO, Takahashi , APPLICANT: SHINTANI, Yasushi	APPLICANT: MIYAJIMA, No. US20040029793Aluyuki TITLE OF INVENTION: No. US20040029793Alel G Protein-Coupled Receptor Protein and its FILE REFERENCE: 2737 USOP CURRENT APPLICATION NUMBER: US/10/297,908A	CURRENT FILING DATE: 2002-12-11  PRIOR APPLICATION NUMBER: PCT/JP01/05061  PRIOR FILING DATE: 2001-06-14  PRIOR APPLICATION NUMBER: JP 2000-184596	PRIOR FILING DATE: 2000-06-15 PRIOR PLILOGATION NUMBER: JP 2000-223887 PRIOR FILING DATE: 2000-07-19 NUMBER OF SEQ ID NOS: 7	; SEQ ID NO Z ; LENGTH: 918 ; TYPE: DNA ; ORGANISM: Human

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100.0%; Score 918; DB 9; Length 918;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 918; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 918
                                                                                              TYPE: DNA
CRGANISM: Homo sapiens
US-09-995-225-3
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901 TGTGTTTTGTGCCGTTAG 918
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 1, Applisequence 54, Applisequence 7, Applisequence 7, Applisequence 135, Applisequence 135, Applisequence 23, Applisequence 23, Applisequence 135, Applisequence 165, Applisequence 23, Applisequence

Sequence 24, Appl Sequence 25, Appl Sequence 24, Appl Sequence 55, Appl Sequence 112, App Sequence 3, Appli Sequence 22, Appli

Sequence Sequence Sequence Sequence Sequence

ALIGNMENTS

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US-09-995-225-3
| Sequence 3, Application UG/09995225
| Sequence 3, Application UG/09995225
| Publication No. USZ02019584A1
| GENERAL INFORMATION|
| APPLICANT: Chen, Ruoping
| APPLICANT: Chen, Ruoping
| APPLICANT: Chu, Zhi Liang
| APPLICANT: Chu, Zhi Liang
| APPLICANT: Chu, Zhi Liang
| APPLICANT: Lowitz, Kevin P. |
| TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G. |
| TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G. |
| TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G. |
| TITLE OF INVENTION: Endogenous And No. US200219388 |
| PRIOR APPLICATION NUMBER: 60/233,404 |
| PRIOR APPLICATION NUMBER: 60/225,366 |
| PRIOR PLING DATE: 2001-02-20 |
| PRIOR PLING DATE: 2001-02-20 |
| PRIOR PLING DATE: 2001-04-66 |
| PRIOR PLING DATE: 2001-04-66 |
| PRIOR FILING DATE: 2001-04-66 |
| PRIOR PLICATION NUMBER: 60/280,356 |
| PRIOR PLICATION NUMBER: 60/280,317 |
| PRIOR PLICATION NUMBER: 60/280,317 |
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                                                                                                                                                                                                                                April 25, 2004, 17:54:09 ; Search time 460 Seconds (without alignments) 8997.651 Million cell updates/sec
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Sequence 1007,
Sequence 1, Ap
Sequence 21, A
Sequence 26, Ap
Sequence 26, Ap
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| cgn2_6/ptodata/2/pubpna/PCT WEW PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_DUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pub
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-297-908A-2
US-10-055-106C-1
US-10-055-106C-1
US-10-293-171-1
US-10-017-161-1193
US-09-782-974C-81
US-10-085-233B-3
US-10-085-233B-3
US-09-9782-974C-21
US-10-085-233B-3
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Ramkumar, J., Tribouley, C.M., Thornton, M., Kallick, D.A., Yao, M.G.,
Bliott, V.S., Burford, N., Khan, F.A., Yue, H., Lu, Y., Arvizu, C.,
Roopa R., Muyen, D.B., Lee, B.A., Lu, D.A., Ison, C.H., Walsh, R.T. and
Polick, J.L.
G-protein coupled receptors
Patent: WO 0226925-A 22 04-APR-2002;
Incyte Genomics, Inc. (US)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="taxon:9666"
/note="Incyte ID No: 6157025CB1"
               GI:21698748
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Homo sapiens (human)
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Matches 906, Conservative
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                         AC146385
Pan troglodytes chromosome UNK clone RP43-126C6, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 164055)
Wilson,R.K.
                                                                                                                                                                                                                                                                                    Sequencing Center, 4444
USA
                                                                                                                                                                                                                                                                                                                                                              Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, NO 63108, USA on Nov 4, 2003 this sequence version replaced gi:33620890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
Center code: WGSC
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/note="assembly_name:Contig3"
24986. .66573
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66674. .164055
/note="assembly_name:Contig5"
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2 (bases 1 to 164055)
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="UNK"
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                                                                        AC146385
AC146385.2
GI:38154073
HTG; HTGS PHASE1.
Pan troglodytes (chimpanzee)
Pan troglodytes
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Submitted (13-AUG-2003) G
Forest Park Parkway, St.
3 (bases 1 to 164055)
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Score 913.2; DB 2;
Pred. No. 5.2e-224;
0; Mismatches 3;
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AX451925
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DEFINITION
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QEFWAQLKNLFFIGVILVCFLPYQFFRIYYLNVVTHSNACNSKVAFYNBIFLSVTAIS CYDLLLFVFGGSHWFKQKIIGLMNCVLCR" ORIGIN	Query Match 99.8%; Score 916.4; DB 6; Length 1051; Best Local Similarity 99.9%; Pred. No. 4.6e-225; Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	OY 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60	Oy 61 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGTCATTTCCATTCTTTTC 120	121 CTCCTGGTGAAATGAACACCGGTCAGTGACCACCATGGCGGTCATTAACTTGGTGGTG	181 GICCACAGGETITICIGCIGCAGGCCAIITICGCIIGACCICAICAAGAAGACI [	241 TGGATGTTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATCCACATGTAC	QY 301 CTCACGITCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC 360	OY 361 AAAGACAAATTCTACAGAAAACTGCATGCTGCCGGTGCTGGCATGTGG 420	Oy 421 ACGCTGGTGATTGTCGTACCCTGGTTGTCTCCCCGGTATGGAATCCATGAGGAA 480	OY 481 TACAATGAGGAGCACTGTTTTAAATTTCACAAAGAGCTTGCTT	Oy 541 ATCAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG 600	OY 601 GTCTTCATCATTATGTTGATGGTGCAGAAGCTACGCCACTCTTTACTATCCCACCAGGAG 660	OY 661 TICTGGGCTCAGCTGAAAACCTATTITIATAGGGGTCATCCTTGTTTGTTTCCTTCC 720	Qy 721 TACCAGTICTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC 780	781	B41 CTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGATT	DD 900 CITCICITIGICITIGGGGGGGGGGGTTTGGTTTAAGCAAAGATAATTGGCTTATGGAAT 959 QY 901 TGTGTTTTGTGCGTTAG 918	960 TGTGTTTTGTGCCGTTAG 97	
OY 361 AAAGACAAAGTGGAATTCTACAGAAAACTGCATGTGGCTGCCAGTGCTGGCATGTGG 420	421 ACCTGGTGATTGTCATTGTGATACCCCTGGTTGTCTCCCGGTATGGAATCCATGAGGAA 480 133543 ACCTGGTGATTGTCATTGTGATACCCTTGTTGTCTCCCGGTATGGAATCCATGAGGAA 480 133543 ACCTGGTGATTGTCATTGTGATACCTATGTCTTCTCCCGGTATGGAATCCATGAAGAA 13350	481 TACAATGAGGAGTATTTAAATTTTCACAAGAGTTGCTTGC	133603 IACACIDATAGATCATTITIGACATAGACGATIGCIGGATCTCTGTGGGTCTTCCAG 600 133663 ATCAACTATATGATAGTCATTITIGCATAGCCGTTGCTGTGATTCTGTTGGGTCTTCCAG 1337	601 GTCTTCATCATTATGTTGATGGAGAGAGCTACGCCACTCTTTACTATCCCACCAGGAG 	661 TTCTGGGCTCAGCTGAAAACCTATTTTTATAGGGGTCATCCTTGTTTGT	780 13390	840	900	901 TGTGTTTTGTGCCGTTAG 918 	SULT 13	AAA53412 LOCUS DEFINITION Sequence 1 from Patent WO0244212. ACCESSION AA453412 VERSTON AA453412 GT.21712725	Homo sapiens (human) Gram sapiens Gram Sapiens Gram Sapiens	Mammalia; Eutheria; Primates; Cat CE 1 RS Deleersnijder,W., Blockx,H. and d	JITLE Human G-Protein Coupled receptor and uses thereof JOURNAL Patent: WO 0244212-A 1 06-JUN-2002; SOLVAY PHARMACEUTICALS B V (NL)	rce	CDS 60 977 /note="unnamed protein product" /codon start=1 /codon start=1	/procent_const_ /db_xref="G1:2172226" /db_xref="RBMTREMBL:CAD38106"	/translation="MPGHNTSRNSSCDPIVTPHLISLYFIVLIGGLVGVISILFLLVK MNTRSVTTMAVINLVVVHSVPLLTVDPRLITYLIKKTWMFGLPPCKFVSAMLHHMYLT FLFYVVILVTRYLIFPRCKDKVEFYRKLHAVAASAGWMTLVIVVVPLVVSRYGIHEE YNEEHCFKFHKELAYTYVKIINYMIVIFVIAVAVILLVFQVFIIMLMVQKLRHSLLSH	

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ACO83865 218186 bp DNA linear PRI 26-JAN-2001 Homo sapiens chromosome 7 clone RP11-605P22, complete sequence. ACO83865 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. AC083865.2 GI:12545315 sapiens (human) sapiens Homo Ношо ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION RESULT 12 AC083865

Classes 1 to 218186)
Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.
Direct submission
Submitted (04-0CT-2000) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA Direct Submission Submitted (26-DAN-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On Jan 26, 2001 this sequence version replaced gi:10567930. Center project name: HeaChr7

Center Cone name: RP11-605P22 (djs708)

Center Cone name: RP11-605P22 (djs708)

Sequencing vector: plasmid; X52328; 100% of reads
Sequencing vector: plasmid; X52328; 100% of reads
Assembly program: Phrap; version 0.99319

Consensus quality: 217693 bases at least Q40

Consensus quality: 218165 bases at least Q30

Consensus quality: 218165 bases at least Q30

Consensus quality: 218165 bases at least Q30

Consensus quality: 21816 bases; agarose-fp

Quality coverage: 8.30x in Q20 bases; sum-of-contigs 5': mapping in progress 3': RP11-243E12 (UWGC:djs156) AC018634, 6468-bp overlap and Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D.
Olson,M.V. Large-scale Mapping and Sequencing of Human Chromosome Center: University of Washington Genome Center Center Code: UWGC Web site: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu (bases 1 to 218186) to 218186) Overlapping Sequences: Unpublished JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS TITLE TITLE

COMMENT

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank filet file format but are available as part of this entry's ASN:1 file. Sequence Quality Assessment:

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality.>= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

FngrPrnt SeqDerMap BgliISeqDerMap FngrPrnt SegDerMap FngrPrnt

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Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A 1007 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JP); Center for Advanced Science and Technology Incubation, Ltd.
(JP)
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llarity 100.0%; Pred. No. 2.9e-225;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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.larity 100.0%; Pred. No. 1.9e-225;
Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 81 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers

    1. .2525
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
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AX147836
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 020630044 A 54 15-AUG-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Sequence 54 from Patent WO02063004.
AX709195.1 GI:29564789
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Kallick, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S.,
Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, P.A., Walsh, R.T., Ison, C.H.)
Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and
CTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 900
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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iive 0; Mismatches 0;
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|mol_tyre="taxon:9606"
|noTe="Incyte ID No: 90012586CB1"
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Patent: WO 02063004-A 53 15-AUG-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Sequence 53 from Patent WO02063004.
AX709194 1 GI:29564788
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Novel Polypeptide
Patent: JP 2003024082-A 1 28-JAN-2003;
Pfizer Limited (EP (GB) only), Pfizer Inc (EP except GB / U CS Home sapiens
PN JP 2003024082-A/1
PD 28-JAN-2003
PP 23-JAN-2003
PP 23-JAN-2004 GB 0101739.1
PR 23-JAN-2001 GB 0101739.1
PR 23-JAN-2001 GB CC CC FH Key
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Best Local Similarity 100.0%; Pred. No. 1.7e-225;
Matches 918; Conservative 0; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 918)

Fredriksson, R., Hoglund, P.J., Gloriam, D.E., Lagerstrom, M.C. and Schioth, H.B.
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                                                          AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG
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Fredriksson, R., Hoglund, P.J., Gloriam, D.B.I., Lagerstrom, M.C.
Schioth, H.B.
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Submitted (30-APR-2003) Neuroscience, Unit of
University, Box 593, Uppsala 75124, Sweden
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.7e-225;
Matches 918; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens G protein-coupled 1
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us-10-055-106c-1.rge

DD 61 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGTGTCATTTCCATTCTTTC 120		OY 181 GECEACAGCGTTTTCTGCTGACAGTGCCATTCGCTTGACCTACCT		OY 301 CTCACGTTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAGTGG 360	4 4	Qy 421 ACGCTCGTATTGTCGTACCCCTGGTTGTCCCCGGTATGGAATCCATGAGGAA 480  Db 421 ACGCTGGTGATTGTCATTGTGGTACCCCTGGTTGTCTCCCCGGTATGGAATCCATGAGGAA 480	OY 481 TACAATGAGGAGCACTGTTTTAAATTTCACAAAGAGCTTGCTT	OY 541 ATCAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG 600 Db 541 ATCAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG 600	601	OY 661 TICTGGGCTCAGCTGAAAACCTATITITATAGGGGTCATCCTTGTTTGTTTCCTTCC 720	OY 721 TACCAGITCTITAGGAICTAITACTIGAAIGTIGIGAGGCAITCCAAIGCCIGIAACAGC 780 Db 721 TACCAGITCTITAGGAICTAITACTIGAAIGTIGIAGCGCAITCCAAIGCCIGIAACAGC 780	Qy 781 AAGGTIGCATITIATAACGAAATCTICTIGAGTGTAACAGCAATTAGCTGCTATGATITG 840	Qy 841 CTTCTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 900	Oy 901 TGTGTTTGTGCCGTTAG 918	RESULT 4 BD187510 BD187510 918 bp DNA linear PAT 17-JUL-2003		ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 918) AUTHORS Lee, H.
	OY 661 TICIGGGCICAGCIGAAAAACCIAITITITAAAAGGGCICAICCTIGITITGITICCTICC 720	Qy 721 TACCAGITCITTAGGAICIAITACITGAAGGITGIGACGCAITCCAAIGCCIGTAACAGC 780 Db 721 TACCAGITCITIAGGAICIAITACITGAATGTIGACGACGCAITCCAAIGCCIGTAACAGC 780	Qy 781 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTACAACGAATTAGCTGCTATGATTTG 840 Db 781 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTG 840	OY 841 CITCICITIGECENTIGGGAAGCCATIGGTITAAGCAAAAGATAATIGGCITAUGGAAI 900  B41 CITCICITIGGGGGAAGCCATIGGITIAAGCAAAGATAATIGGCITAIGGAAI 900	Oy 901 TGTGTTTTGTGCGTTAG 918  Db 901 TGTGTTTTGTGCGTTAG 918	RESULT 3	BD105324 ON Novel G protein-coupled receptor protein and its DNA. N BD105324 BD105324 BD1:22650898	S WO 0196567-A/1.  Homo sapiens (human) ISM Homo sapiens	0.000	Ţ.	PN WO 0196567-A/1 PD 20-DEC-2001 PF 14-JUN-2001 WO 2001JPD05061 PR 15-JUN-2000 JP 00P 184596,19-JUL-2000 JP 00P 22:	TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUVUKI MIYAJIMA PC C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC A61K38/00, A61K48/00, A61P1/00, A61P3/10, A61P9/00, A61P2/28, PC	1.P2	FT		Query Match Best Local Similarity 100.0%; Pred. No. 1.7e-225; Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60

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                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 918; DB 6; Length 918;
Best Local Similarity 100.0%; Pred. No. 1.7e-225;
Matches 918; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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TGTGTTTTGTGCCGTTAG 918
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Best Local Similarity 100.0%; Pred. No. 1.7e-225;
Matches 918; Conservative 0; Mismatches 0;

    .918
    /organism="Homo sapiens"
    /mol type="unassigned DNA"
    /db_xref="taxon:9606"

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                    FEATURES
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

<sup>41:</sup> em\_ntgo\_other:-Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	p DNA linear 83. Craniata; Vertebrata; Catarrhini; Hominidae; Ox
Length DB ID  918 6 AX498150 918 6 AX498180 918 6 AX498180 918 6 BD105224 918 9 AY298420 1336 6 AX709195 2525 6 AX709195 2525 6 AX709195 11330 6 AX651838 164055 2 AX146385 164055 AX146385 164055 AX146385 164055 AX146386 1651 6 AX709195 2525 6 AX57188 164055 AX16386 164055 AX16386 164055 AX16386 164055 AX16386 164055 AX16386 164055 AX16386 16539 AX28642 47 6 AX57182 447 6 AX52182 16539 AX16462 16539 AX166239 166055 BX660462 1673 AX16239 1673 AX16239 173 AX16642 173 AX166239 173 AX166239 173 AX166239 173 AX166339 173 AX166331310 173 AX166339 173 AX1663	918 b 8P12251 rdata; nates; recept 24-JUL-
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The invention relates to human G-protein coupled receptor (GCREC 1-16) polypeptides and polynucleotides. Sequences of the invention are useful for the diagnosis, treatment and prevention of cell proliferative (e.g. cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris, autoimmune/inflammatory (sheumatoid arthritis, Hashimoto's thyroiditis) and metabolic disorders (e.g. obesity, osteoporosis), viral infections, atheroselerosis and hepatitis. GCREC proteins are useful for identifying compounds that modulate, mimic and block olfactory and taste sensations. They are also useful for identifying GCREC modulators. GCREC DNAS are
                                                   Human; G-protein coupled receptor-6; GCREC-6; atherosclerosis; cancer; cell proliferative disorder; gastrointestinal; autoimmune; metabolic; neurological; inflammatory; cardiovascular; viral infection; anorexia; cirrhosis; multiple sclerosis; Huntington's disease; gene therapy; Alzheimer's disease; heart failure; hepatitis; cholecystitis; obssity; rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris; osteoporosis; gene; ss.
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Tribouley CM, Thornton M, Kallick DA, Yao MG;
Burford N, Khan FA, Yue H, Lu Y, Arvizu C, R
Lee EA, Lu DAM, Ison CH, Walsh RT, Policky JL;
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(GCREC-6) cDNA
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13-CCT-2000; 2000US-0240589P.

20-CCT-2000; 2000US-0243223P.

03-NOV-2000; 2000US-0245855P.

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P-PSDB; AAE23414.
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Best Local Similarity:
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Anti-HIV; cytostatic; antidiabetic; antiasthmatic; antiinflammatory; haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic; antibacterial; virucide; fungicide; analgesic; antipactrinana; GPCR; cardiant; dermatological; antiinfertility; hepatotropic; antiallergic; antipacatic; ophthalmologial; antianginal; antithyroid; anticonvulsant; antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I; antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I; skeletal; bone metabolism disorder; bone marrow mononuclear disorder; cellular proliferative; differentiative disorder; hormonal disorder; neurological disorder; cardiovascular disorder; inver disorder; ancer; cardiovascular disorder; viral disease; pain; liver disorder; cardiovascular disorder; viral meningitis; fungal meningencephalitis; multiple solerosis; will meningitis; fungal meningencephalitis; multiple solerosis; HIV; wiral meningitis; fungal meningencephalitis; multiple solerosis; Huthington's disease; hart failure; angina pectoris; dermatitis; myocardial infarction; rheumatold arthritis; psoriasis; Crohn's disease;
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The invention relates to an isolated polypeptide, which is a G-protein coupled receptor (GPCR) related to Subfamily I of G-protein coupled receptor (GPCR) related to Subfamily I of G-protein coupled receptor type proteins (GPCRs), designated the 93870 receptor. The polypeptides nucleic acid molecules and antibodies of the invention are useful in screening assays, predictive medicine (e.g. diagnostic assays, compilerative midle in the prophylactic). They are useful in creating and diagnosing conditions related to aberrant activity or expression of the 93870 polypeptides or nucleic acids, e.g. immune and inflammatory disorders, platelet disorders, skeletal or bone metabolism disorders, or bone marrow mononuclear disorders, as well as cellular proliferative and/or differentiative disorders, hormonal disorders, nucled cancer, disbetes mellitus, hypothyroidism, can be reaching and pain and metabolic disorders. Conditions that can be treathyroidism, reproductive or fertility disorders, HIV, bacterial or viral meningitis, fungal meningencephalitis, multiple sclerosis, hyperthyroidism, reproductive or fertility disorders, HIV, bacterial or viral meningitis, fungal meningencephalitis, multiple sclerosis, HIV alterner's disease, Parkinson's disease, axis axia-telanglectasia, enthancer of disease, parkinson's disease, axis axia-telanglectasia, chifarmatory bowel disease, asthma, conjunctivitis, graft-versus-host disease, asthma, espinance or osteoporosis. The transgenic animals are useful for studying the function and or indentifying and/or evaluating medicides heart invention can be used in the herapy. This polymucleotide sequence represents the cDNA of the invention.
                                                                                                          Location/Qualifiers
147. .1088
/*tag= a
//product= "Human G-protein coupled receptor type protein
93870"
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inflammatory bowel disease; asthma; graft-versus-host disease; allergy; conjunctivitis; idiopathic thrombocytopenia; osteoporosis; gene therapy; transgenic animal; human; gene; ss.
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P-PSDB; AAO22919.
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Sequence 1684 BP; 435 A; 366 C; 351 G; 531 T; 0 U; 1 Other;

1684 304

Length:

Matches: Conservative: Mismatches: Indels: Gaps:

4.03e-128 1587.00 100.00\$ 99.67\$ 99.69\$

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

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93870"
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                                                                                  221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro
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The invention relates to an isolated polypeptide, which is a G-protein coupled receptor (GPCR) related to Subfamily I of G-protein coupled coupled receptor type proteins (GPCR), designated the 3840 receptor. The polypeptides, nucleic acid molecules and antibodies of the invention are polypeptides, nucleic acid molecules and antibodies of the invention are controling clinical trials or pharmacognetical), or in methods of treatment (e.g. therapeutic and prophylactic). They are useful in treatment (e.g. therapeutic and prophylactic). They are useful in treatment (e.g. therapeutic and prophylactic). They are useful in the 1847 properties or nucleic acids. e.g. immune and inflammatory disorders, platelet disorders, skeletal or bone metabolism circliammatory disorders, platelet disorders, when a sellular confiscative and pain and metabolic disorders, hormonal disorders, neurological disorders, cardiovascular disorders, viral diseases, liver disorders, and pain and metabolic disorders. Conditions that can be reated include cancer, diabetes mellitus, hypochyroidism, reproductive or fertility disorders, HIV, bacrerial or viral meningitis, fungal meningoencephalitis, multiple sclerosis, hyperthyroidism, reproductive or fertility disorders, HIV, bacrerial or viral meningitis, fungal meningoencephalitis, multiple sclerosis, Huntington's disease, heart failure, angina pectoris, myocardial circliam. reproductive or fertility dermatitis, psoriasis, Crohn's disease, allergy, idiopathic thrombocytopenia, or osteoporosis and infarmatory bowel disease, asthma, conjunctivitis, graft-versus-host circlianses, allergy, idiopathic thrombocytopenia, or osteoporosis of a 93870 protein and for identifying and/or evaluating modulacrs of a 1830 protein and for identifying and/or evaluating modulacrs of a 1830 protein and for identifying and/or evaluating modulacrs of a 1830 protein and for identifying and or or observation or one bused in content and evaluating condition or servation or gene therapy. This polymocleotide sequence represents
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                                                                                                                                              CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC
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The invention discloses an isolated human polypeptide, and encoding nucleic acid, for a G protein-coupled receptor (GPCR), particularly the nucleic acid, for a G protein-coupled receptor (GPCR), particularly the communication between calls and their environment and are characterised by a serpentine structure that passes through the ceall membrane seven times hence the reason such receptors are sometimes called seven transmembrane receptors (TTM). The polymuclectides and polypeptides are useful for identifying an index and polymuclectides and polypeptides are the polypeptide or in the polypeptide for identifying an index and that binds the polypeptide or polymuclectide and/or modulates its biological activity, for screening at the polymoclectide and/or modulates its biological activity, for screening a compound useful for a genetic prediposition to the disorder, for identifying compounds useful for the treatment of a mental disorder, for identifying compounds useful for the treatment of a mental disorder, for identifying compounds useful for the treatment of a mental disorder, for identifying an immune response in a mammal. The nucleic acid or negul for inducing an immune response in a mammal. The nucleic acid or polypeptide is particularly useful, using gene therapy, for treating e.g. anxiety disorders, depression, bipolar disorder, schizophrenia, huntington's disease, dyskinesias, manic depression, stroke, Parkineson's be used for treating diabetes, inflammation or wounds. The sequences presented in ABS70202-ABS70248, ABS70338 and ABS70243 are the DNAs conding the nGPCRs (also referred to as beGPCRs)

nucleic acids and polypeptides of the nG protein-coupled receptor, ful for treating or diagnosing a mental disorder or a disorder seting the brain, e.g. anxiety disorders, schizophrenia, stroke or

Example 1; Page 84-85; 244pp; English

Parkinson's disease.

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14-FEB-2001; 2001WO-US004641. 14-FEB-2001; 2001WO-US004641.

WO200264789-A1.

22-AUG-2002

(PHAA ) PHARMACIA & UPJOHN

(1-2525)US-10-055-106C-2 (1-305) x ABS70242

146 206 98 40 9 Archaccicitationing LeuLeuVallysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuValVal 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProlleValThrProHisLeu 21 IleSerLeuTyrPhelleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe 27 87 41 147 ઠે 셤 ò g ઠ g

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ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr

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wound;

Human, gene, ds, G protein-coupled receptor; GPCR; nGPCR; beGPCR; nG protein coupled receptor; communication; serpentine structure; seven transmembrane receptor; 7TM; mental disorder; diagnosis; genetic predisposition; brain; immune response; gene therapy; anxiety disorder; depression; bipolar disorder; schizophrenia; Huntington's disease; dyskinesia; manic depression; stroke; Parkingon's disease; Alzheimer's disease; diabetes; inflammation;

Homo sapiens tranquiliser

human G protein-coupled receptor, nGPCR-16.

encoding

(first entry)

26-NOV-2002

ABS70242;

ВЪ

DNA; 2525

ABS70242 standard;

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leuleupheValpheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
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                                                        AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGTGGCTGCCAGTGCTGGGATGTGTGG
                                                                                  141 ThrLeuVallleVallleValValProLeuValValSerArgTyrGlylleHisGluGlu
                                                                                                ValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHisGlnGlu
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CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAGTGC
                                  LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp
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99US-0166071P.
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17-NOV-1999;
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The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 21-18, 40, 41, 53-60) and their codding sequences. The present sequence is the coding sequence for one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transmembrane receptors and function in signal than the diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for creening a human to diagnose a disorder affecting the brain or a genetic confermitying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a diagnostic tool for diseases or constitution of sorders infections such as HIV-I, metabolic and cardiovascular diseases, proliferative disorders, renal failure, rheumatoid arthritis, or nordering such as HIMPADD (attention deficit hyperactivity disorder attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Alzheimer's disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders cancers.
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Bannigan CM, Ruff V, Sejlitz T, Huff I
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19-NOV-1999; 99US-0166678P.
28-EEB-2000; 2000US-018123P.
28-FEB-2000; 2000US-0185421P.
28-FEB-2000; 2000US-018554P.
28-FEB-2000; 2000US-018554P.
28-FEB-2000; 2000US-018554P.
39-MAR-2000; 2000US-0186811P.
17-MAR-2000; 2000US-0190810P.
21-MAR-2000; 2000US-0190800P.
21-MAR-2000; 2000US-0190800P.
21-MAR-2000; 2000US-0190800P.
22-MAY-2000; 2000US-020119P.
25-MAY-2000; 2000US-020111P.
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Schellin KA, Kaytes PS, Ba
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P-PSDB; AAG80969.
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                                                  CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC
                                                                              LysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrp
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This invention describes novel polypeptides which have anti-HIV, hepatcherotecine, cytostatic, neuroprotective, antiparkinsonian, hepatchtropic, laxative, cerebroprotective, antiinflammatory, virucide, antibacterial, fungicide and protozoacide activity. The products of the invention are useful for treating a disease or condition associated with decreased expression or over expression of functional G-protein coupled receptors (GCREC), will antibodies generated against the polypeptide of with the expression of GCREC e.g. arterioscelerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease, Constipation, AIDS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy. AAPR988807-encode the GCREC proteins represented by AAB71322-AAB71369, described in the disclosure of the invention
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                                                                                                                                                  Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
Kallick DA, Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalla A,
Ramkumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;
Garaul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
Warren BA, Yang J, Lee EA, Harland L;
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                                                                                                                                                                                                                                                                                                      New human G-protein coupled receptors (GCREC), useful for diagnosing treating a disease or condition associated with decreased expression over expression of functional GCRECs e.g. cancer, Alzheimer's and Parkinson's.
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Conservative:
Mismatches:
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23-PEB-2001; 2001US-0271215P.
08-MAR-2001; 2001US-0274551P.
23-MAR-2001; 2001US-0278507P.
30-MAR-2001; 2001US-0280597P.
02-APR-2001; 2001US-0281107P.
06-APR-2001; 2001US-0281121P.
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P-PSDB; AAB71327.
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2002WO-US003635

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CTTCTCTTTGTCTTTGGGGGGAAGCCATTGGTTTAAGCAAAAAGATAATTGGCTTATGGAAT 1118
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This invention describes novel polypeptides which have anti-HIV, antipateriosclerotic, cytostatic, neuroprotective, antiparkineonian, hepatetropic, laxative, cerebroprotective, antiinflammatory, virucide, antibacterial, fungicide and protozoacide activity. The products of the invention are useful for treating a disease or condition associated with decreased expression or over expression of functional G-protein coupled recepcors (GCREC), while antibodies generated against the polypeptide of the invention are useful for diagnosing a condition or disease associated with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer, stroke, Alabaimer's disease, parkinson's disease, Crohn's disease, stroke, Alabaimer's disease, parkinson's disease, Crohn's disease, constipation, ALDS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy. AAB781359, described in the disclosure of the invention
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                                                                                                                                                                                                                        Tribouley CM, Nguyen DB, Thornton M, Yao MG;
Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia .
Pei J, Tang Yr, Yue H, Reddy R, Butford N, Lu DAM;
Khan FA, Walsh Kr, Ison CH, Richardson TW, Griffin JA
Yang J, Lee EA, Harland L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 114; Page 213; 239pp; English.
                                              2001US-0267322P.
2001US-0271215P.
2001US-0274551P.
2001US-0278507P.
2001US-0280597P.
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                                                                 23-FEB-2001;
08-MAR-2001;
23-MAR-2001;
30-MAR-2001;
02-APR-2001;
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Ramkumar J,
Graul RC, KJ
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Parkinson's.
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This invention describes novel polypeptides which have anti-HIV, antiparkinesorleriotic, cytostatic, neuroprotective, antiparkinesonian, hepatotropic, laxative, cerebroprotective, antiparkinesonian, antibacterial, fungicide and protozoacide activity. The products of the invention are useful for treating a disease or condition associated with decreased expression of functional G-protein coupled receptors (GCRC), while antibodies generated against the polypeptide of the invention are useful for diagnosing a condition or disease associated with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease, constitation, ALS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy.

AAF88580-AAF88627 encode the GCREC proteins represented by AAB71322-
                                                                                                                                                                                                                                                                                                                                                                        Tribouley CM, Nguyen DB, Thornton M, Yao MG; Gandhi AR, Walia NK, Arvizu C, Ellict VS, Hafalia AJA; Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM; Khan FA, Walsh FT, Ison CH, Richardson TW, Griffin JA; Yang J, Lee EA, Harland L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGTGTCATTTCCATTCTTTTC
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08-MAR-2001, 2001US-0274551P.
23-MAR-2001, 2001US-0278507P.
30-MAR-2001, 2001US-0280597P.
02-ARR-2001, 2001US-0281107P.
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Best Local Similarity:
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                         WO200263004-A2
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Kallick DA,
Ramkumar J,
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                                                                   15-AUG-2002
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Warren BA,
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Location/Qualifiers 60. .977

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Novel G-protein coupled receptor IGS70 polypeptide useful for treating dysfunctions, disorders or disease related to lung, bone marrow, spinal cord immune system.
                                                                                                                                                                                                                                                    Claim 1; Page 6; 58pp; English.
                                                                                        23-NOV-2001; 2001WO-EP013706
                                                                                                           30-NOV-2000; 2000EP-00204280
05-DEC-2000; 2000US-0251045P
                                                                                                                                                            Deleersnijder W, Blockx H,
                                                                                                                                       (SOLV ) SOLVAY PHARM BV
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P-PSDB; AAU99179.
                                                 WO200244212-A2
Key
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De Moor L;

The invention relates to a G protein-coupled receptor (GPCR) IGS70

Co polypeptide including sequences that are 98-99.6% identical. Also

Included are the polymucleotide encoding IGS70 (including sequences 9999.6% identical to the polymucleotide or the DNA insert contained in

Description of the polymucleotide or the DNA insert contained in

CC 99.6% identical to the polymucleotide or the DNA insert contained in

CC 99.6% identical to the polymucleotide or the DNA insert contained in

CC 000 principleotide a DNA or RNA expression system producing IGS70, a host

CC comprising the expression system, IGS70 receptor membrane preparation

CC 000 describe or the cell, an antibody immunospecific for IGS70, IGS70 is

CC 000 subject related to expression or activity of the IGS70 polypeptide in a

CC 000 subject by determining the presence or absence of mutation in the

CC 000 subject by determining the presence or absence of the subject in a

CC 000 subject the subject IGS70 is also useful identifying agonist

CC 00 antagonist are useful for treating psychiatric and central nervous

CC 00 antagonist are useful for treating psychiatric and central nervous

CC 00 antagonist anxiety, cardiovascular diseases such as heart

CC multiple sclerosis, myocadial infarction, kidney disease uch as

CC multiple spatrointesthal disorders such as irritable bowel

CC renal failure, gastrointesthal disorders such as irritable bowel

CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,

CHIV), diabetes, osteporosis and allergies, The present sequence encodes

CC the human GPCP IGS70 60 AIGCCIGGCCACAATACCICCAGGAAITCCTCTIGCGAICCTATAGIGACACCCCACTIA 1 MetProGlyHisAsnThrSerArgAsnSerSerCysAspProIleValThrProHisLeu 21 IleSerLeuTyrPheileValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other; Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-055-106C-2 (1-305) x ABK87351 (1-1051) 8.76e-129 1592.00 100.00% 100.00% Similarity: human GPCR Percent Similarity: Query Match: DB: ò ద ò

> Human; ss; gene; G protein-coupled receptor; GPCR; IGS70; CNS; gene; deptoriation disorder; central nervous system disorder; schizophrenia; Alzheimer's disease; multiple sclerosis; anxiety, cardiovascular disease; heart failure; angina pectoris; myocardial infarction; kidney disease; renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS; inflammatory bowel disease; ulcer; inflammation; cancer; asthma; infection; human immunodeficiency virus infection; HIV; diabetes; osteoporosis, allergy.

Homo sapiens

Human cDNA encoding G protein-coupled receptor IGS70.

(first entry)

24-SEP-2002

ABK87351;

ABK87351 standard; cDNA; 1051 BP

179 9

LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaVallleAsnLeuValVal

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New GAVE18 polypeptide and nucleic acid molecule encoding the polypeptide, useful for preventing and treating a disease or disorder associated with aberrant expression or activity of GAVE18, e.g. asthmathematoid arthritis.
                   ocation/Qualifiers
                                       /*tag= a
/product= "GAVE18
                                                                                                                                                                               Busch
                                                                                                                                                                                                                                                                                  Claim 1; Fig 5; 88pp; English.
                                                                                                                             13-NOV-2001; 2001US-0354150P.
22-MAR-2002; 2002GB-00006891.
                                                                                                           08-NOV-2002; 2002WO-US035887
                                                                                                                                                             (AVET ) AVENTIS PHARM INC.
                                                                                                                                                                               Eishingdrelo H, Cai J,
                                                                                                                                                                                                  WPI; 2003-457496/43.
P-PSDB; AAO27265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                    WO2003042399-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
 Homo sapiens
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This invention relates to a novel G-protein coupled receptor (GAVE18)

that is involved in signal transduction in respect to inflammation and

the physiological immunological response. Molecules which may modulate

the signalling activity or signal transduction of the receptor may be

antinflammatory, antiasthmatic, antirheumatic or antiarthritic. The

GAVE18 receptor and the DNA sequence encoding it may be a target for

antisense therapy or gene therapy. The nucleic acid molecule, GAVE18

proteins and antibodies may be useful in screening assays, detection

assays (for example chromosomal mapping, tissue typing or forensic

blology), or predictive medicine (for example diagnostic assays,

consostic assays, monitoring cilnical trials and pharmacogenomics. The

prognostic assays, monitoring cilnical trials and pharmacogenomics. The

goonist and antagonist are also useful for preventing and treating a

disease or disorder associated with aberrant expression or activity of

GAVE18, such as inflammation and immunological-related diseases or

checkers, for example asthma, chronic obstructive pulmonary disease or

rheumatoid arthritis. The present sequence is the DNA sequence encoding

the GAVE18 protein of the invention
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disease; COPD;

Human G-protein coupled receptor; GAVE18; signal transduction; inflammation; physiological immunological response; antiinflammatory; antiasthmatic; antirheumatic; antiarthritic; antisense therapy; chromosomal mapping; tissue typing; forensic biology; predictive medicine; asthma; chronic obstructive pulmonary disease; Cheumatoid arthritis; gene; ds.

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The invention provides new G-protein coupled receptor (GPCR) polypeptides designated TGR2, TGR38, TGR18, TGR164, TGR343 and TGR358 and encoding polynucleorides. The polypeptides can be expressed by stendard DNA recombination methodology. The polypeptides are useful for screening or identifying modulators of GPCR or signal transduction. The modulators of signal transduction are useful for treating or preventing TGR-associated disorders, e.g. asthma, multiple sclerosis or kidney disease. The polypeptides are useful as targets for diagnosing or treating e.g. epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia, esymptomatic urinary abnormalities, hypertension, nephrolithiasis, cirrhosis, lesions, jaundice, psoriasis, lupus erythematosus, or acute inflammatory dermatoses. The present sequence represents a human TGR343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New G-protein coupled receptor polypeptides designated TGR2, TGR38, TGR18, TGR164, TGR343 and TGR358, useful as targets for screening drugs for treating or preventing e.g. asthma, multiple sclerosis, stroke or nephrolithiasis.
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                                                                                              G-protein coupled receptor; GPCR; TGR38; TGR118; TGR164; TGR343; TGR358; antiasthmatic; neuroprotective; cerebroprotective; nephrotropic; anticonvulsant; hypotensive; hepatotropic; dermatological; human; immunosuppressive; antiinflammatory; gene; ds.
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                                                  protein encoding DNA
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P-PSDB; ABP71378.
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Best Local Similarity:
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                                                     Human TGR343
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The present invention provides the protein and coding sequences of several human G-protein coupled receptors (GPCRs). These can be used in the identification of candidate compounds as receptor agonists or inverse agonists having applicability as therapeutic agents. The present sequence is a GPCR coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                      Human, G-protein coupled receptor; GPCR, hRUP28; hRUP29; hRUP30; hRUP31; hRUP31; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
                                                LeuleuPheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel endogenous and non-endogenous versions of G protein-coupled receptor useful for identification of candidate compounds as recepagonists or antagonists for use as therapeutic agents.
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12-DEC-2000; 2000US-0255366P.
20-FEB-2001; 2001US-0270266P.
20-FEB-2001; 2001US-0270286P.
06-APR-2001; 2001US-0282356P.
06-APR-2001; 2001US-0282356P.
06-APR-2001; 2001US-0282356P.
14-MAY-2001; 2001US-0290317P.
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 Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA libraries from peripheral blood mononuclear cells. Two ESTS have been identified in libraries derived from breast mRNA. PFI-021 and the corresponding cDNA are used to treat a patient needing altered activation or expression of a GPCR, such as inflammation, allergy and respiratory, neurology, psychology, urogenital disease, reproductive and sexual dysfunction/disorders, cancer, tissue repair, dermatology, skin pigmentation disorders, photoageing, frailty, osteoporosis, metabolic disease, cardiovascular disease, gastro- intestinal disease, anti-infection, sensory organ disorders, sleep disorders and hair loss
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                                                                                                                  Human testis-originated G protein-coupled receptor protein TGR10 and encoded DNA, useful for gene diagnosis and developing drugs to treat diseases of central nervous system, inflammations and diseases of
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Human, testis-originated G-protein coupled receptor; TGR10; inflammatory; cytostatic; immunomodulator; cardiant; neuroprotective; gene therapy; inflammation; nervous system disease; circulatory system disease; cancer; metabolic disease; immunological disease; gastrointestinal disease; gene;
Human GCR
Human nGP
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Human GPC
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NOUSE G-P
Human GPC
Human CON
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Abz42812 H
Aas98046 H
Abx76412 I
Abx76202 I
Abz78126 H
                               Abs70242 PAG(86524 FAG(86524 FAG(865
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ADB74251
AAH47235
AAH16527
AAF81543
AAF82359
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ADB74248
ADB74249
                                                              AAL53414
AAL53413
AAD37670
ADC12789
ADB78584
AAH50979
ABS70212
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AAK56763
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19-JUL-2000; 2000JP-00223887
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   AAL44713;
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AAL44713
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Aba00160 PFI-021 c
Abc04867 Human G p
Abz59471 Human G-P
Abx87351 Human G-P
Abx87351 Human G-P
Aaf88583 Human GCR
Aaf88584 Human GCR
                                                                                                             April 25, 2004, 18:01:50; Search time 447 Seconds (without alignments) 2898.659 Million cell updates/sec
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1 MPGHNTSRNSSCDPIVTPHL......GGSHWFKQKIIGLMNCVLCR 305
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                     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                 nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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ABZ59171
AAL57070
ABK87351
AAF88583
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Result No.

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Search completed: April 25, 2004, 21:29:30 Job time : 4525 secs

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Baughn, M.R., Graul, R.C., Walia, N.K., Gandhi, A.R., Hafalia, A.J.,
Ramkumar, J., Tribouley, C.M., Thornton, M., Kallick, D.A., Yao, M.G.,
Bliott, V.S., Burford, N., Khan, F.A., Yue, H., Lu, Y., Arvizu, C.,
Roopa, R., Wuyven, D.B., Lee, E.A., Lu, D.A., Ison, C.H., Walsh, R.T. and
Policky, J.L.
G-protein coupled receptors
Patent: WO 0226825-A 22 04-APR-2002;
Incyte Genomics, Inc. (19)
                                                                                                         PAT 03-JUL-2002
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                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
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Indels:
Gaps:
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                                    CysValLeuCysArg
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Matches:
Conservative:
Mismatches:
Indels:
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CTICICITIGECTITGGGGGAAGCCATIGGITTAAGCAAAAGATAATIGGCTTAIGGAAT 134022 CysvalleucysArg 305 	164055 bp DNA linear HTG 04-NOV-2003 tes chromosome UNK clone RP43-126C6, *** SEQUENCING IN ; 3 unordered pieces.	(chimpanzee) coa, Chordata, Craniata, Vertebrata, Euteleostomi, ita, Primates, Catarrhini, Hominidae, Pan. 64055)		re tre	Louis, MO 63108, USA noce version replaced gi:33620890.	Center: Washington University Genome Sequencing Center Center code: WUGSC Web Site.http://genome.wustl.edu/gsc/index.shtml	Center project name: C_PT126C06	Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads	162205 bases at least Q40 162489 bases at least Q30 162744 bases at least Q30	working draft, sequence. It currently nitigs. The true order of the pleces their order in this sequence record is	arbitrary, daps between the contraga are represented as Thins of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will	eserver 1 24885: contig of 24885 bp in length 886 24985: gap of unknown length 986 66573: contig of 41588 bp in length	5: Sopi of unknown length. Qualifiers 5:	Organism = ran crossory (mol type="genomic DN"" (db_xref="taxon:9598" chromosome="UNK"	CIONE="KP43-126C6" 24885
8084 Db 133963 640 Db 134023	SULT 14 146385/C CUS AC146385 PINITION Pan troglodytes PROGRESS ***, 3 RESION AC146385, 91:3 RAION AC146385, 91:3 RAION AC146385, 91:3	REFERENCE 1 133182 HTG. HTG. HTG. HTG. HTG. HTG. HTG. HTG.	40 AUTHORS 133242 TITLE JOURNAL 60 REPERRENCE 60 AUTHORS TITLE	### ##################################	COMMENT  COMMENT  COMMENT	SECYB 120       AGTGC 133482	itTrp 140       GTGG 133542	uglu 160       \GGAA 133602	SEILE 180	rccAG 133722	Inglu 220 **	uDro 240 **	# 66	ppleu 280       hTTG 133962	rogen 300 misc feature 1
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

This sequence bas been validated by Multiple Complete Digest fing sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally darived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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leuleuphevalphedlyGlySerHisTrpPheLysGlnLysIleIleGlyLeuTrpAsn 300
                                      AC083865 218186 bp DNA linear PRI 26-JAN-2001
HOMO Sapiens chromosome 7 clone RP11-605P22, complete sequence.
AC083865 AC083865.2 GI:12545315
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I (Dases 1 to 218186)
Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and Olson, M.V.
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Submitted (26-JAN-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jan 26, 2001 this sequence version replaced gi:10567930.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UMGC
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                                                                                                                                                        12260 TACCAGTICTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
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          PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro
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2 (bases 1 to 218186)
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2 (bases 1 to 2018186)
3 (bases 1 to 2018186)
4 (bases 1 to 2018186)
5 (bases 1 to 2018186)
6 (bases 1 to 2018186)
8 (bases 1 to 218186)
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3': RP11-243E12 (UWGC:djs156) AC018634, 6468-bp overlap
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Center project name: RP11-605P22 (djs708)

Center clone name: RP11-605P22 (djs708)

Sequencing vector: plasmid; X52328; 100% of reads
Sequencing vector: plasmid; X52328; 100% of reads
Assembly program: Phrap, version 0.99019

Consensus quality: 217693 bases at least Q40

Consensus quality: 218145 bases at least Q30

Consensus quality: 218145 bases at least Q30

Consensus quality: 218145 bases at least Q30

Insert size: 273875; 19.1% error; agarose-fp

Insert size: 218186; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Project Information
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ValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeuIleLysLysThr 80		Db 447 ACGCTGGTGATTGTCATTGTGGTACCCCTGGTTGTCTCCCGGAATCCATGAGAAA 506  Cy 161 TyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrValLysIle 180  Db 507 TACAATGAGGAGCACTGTTTTAAATTTCACAAAAGAGCTTGCTT	Oy 181 IleAenTyrMetIleValIlePheValIleAlaValIleLeuLeuValPheGln 200	21 ValPheileileMetteuwervaldinLyaleutrghisSerLeuLeussrhisGinGlu 220  22 PherralacineLiyaRanLeuPhepheileGlyvalileLeuvalCysPheLeuPro 240  23 PherralacineLiyaRanLeuPhepheileGlyvalileLeuvalCysPheLeuPro 240  24 TyrcGacCrcGAGAAACCTATTTTTATAGGGGCTCATCTTTTCTTCCTTC
Oy 181 IleAsnTyrMetIleValIlePheValIleAlaValAlaValIleLeuLeuValPheGln 200	241 TyrdlnPhePheArgileTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer [	807 AAGGTTGCAITTTAIAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTA 281 LeuleupheValPheGlyGlySerHisTrpPheLysGlnLysIleIleGlyLe 867 CITCTTTGGGGAAGCCAITGGTTTAAGGAAAGATAATTGGCT	Oy 301 CysValleuCysArg 305 	AKS21885   AKSZ1885   AKSZ1885

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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 81 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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Sequence 81 from Patent W00136473.
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Qy         241 TyrGlnPhePheArg1leTyrTyrLeuAsnValThrHisSerAsnAlaCysAsnSer 260           Db         939 TACCAGTTCTTTAGGACTTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTACAGC         998           Qy         261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu 280           Db         999 AAGGTTGCATTTATAAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTG 1058           Qy         281 LeuLeuPheValPheGlyGlySerHisTtpPheLysGlnLysIleIleGlyLeuTrpAsn 300           Db         1059 CTTCTTTGTCTTTGGGGGGAAGCCATTGGTTTAAGCAAAAGATATTGGAAT 1118           Qy         301 CysValLeuCysAxg 305           Db         1119 TGGTTTTGGCGT 1133	RESULT 8  AX709194  AX7091	TITLE Harland, L. TOURINAL Parent: WO 02063004-A 53 15-AUG-2002; JOURNAL Parent: WO 02063004-A 53 15-AUG-2002; Incyte Genomics, Inc. (US) FEATURES Location/Qualifiers Location/Qualifiers / no.1.40 / organism="Homo sapiens" / mol.Lype="unassigned DNA" / do xref="texon:9606" / no.1.exon:9606" / no.1.exon:9606"	Alignment Scores.  Pred. No.:  1592.00  Matches:  1592.01  Matches:  Percent Similarity:  100.00\$  Mismatches:  0  Best Local Similarity:  100.00\$  Mismatches:  0  Best Local Similarity:  100.00\$  Mismatches:  0  100.00\$  Mismatches:  100.00\$  Mismatches:  100.00\$  Mismatches:  100.00\$  Mismatches:  100.00\$  Midli

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Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R., Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H., Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and Harland, L. G-protein coupled receptors Patent: Wo 0.0263004-A 52 15-AUG-2002; Incyte Genomics, Inc. (US)
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/orlype="unassigned DNA"
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/noTe="Incyte ID No: 90012430CB1"
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PAT 04-APR-2003

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AX709193 Sequence 52 from Patent AX709193 AX709193.1 GI:29564787

Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallick, D.A., Gandhi, A.R., Walia, N.K., Arvizu, C., Elliott, V.S.,

REFERENCE AUTHORS

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| / db_zref="taxon:9606"
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| FLFYVILVTRYILFFKCKDKVBFYRKLHAVAASAGNWTLVIVVPLVVSRYGIHEE
| YNBEHCFRHYKELAYTYVKIINYMIVIFVIAVAVILLYFQVFIIMLMVQKLRHSLLSH
| QEFWAQLKNLFFIGVILVOTEPYOPFRIYTLNVTHSNAGNSKVAFFYNEIFLSH
| QEFWAQLKNLFFIGVILVOTEPYOPFRIYTLNVTHSNAGNSKVAFFYNEIFLSH
| CKDLLLFVPGGSHWFKQKIIGLMNCVLCR"
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                                                                                                              221 PheTrpAlaGlnLeuLyaAsnLeuPhePheIleGlyValIleLeuValCysPheLeuPro
                                                                   661 freneggereagergaaaacerarrrrrraaaggggreareerrgrrrgrreerree
                                                                                              TyrGlnPhePheArg11eTyrTyrLeuAsnValValThrHisSerAsnAlaCysAsnSer
                                                                                                                                                    LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Human g-protein coupled receptor and uses thereof
Patent: Wo 0244212-A 1 06-JUN-2002;
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 y, Box 593, Uppsala 75124, Sweden
Location/Qualifiers
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(C12N1/21,C12R1:19)
Novel G protein-coupled receptor protein and its DNA FH Key
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A61K45/00, A61K48/00, A61P1/00, A61P3/10, A61P9/00, A61P25/28,
                                                                           Location/Qualifiers
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/db_xref="taxon:9606"
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1 (bases 1 to 918)

2 Moriya,T. Ito,T.; Shintani,Y. and Miyajima,N.

Novel G protein-coupled receptor protein and its DNA

1. Patent: WO 0195657-A 1 20-DEC-2001;

2 Patent: WO 0195657-A 1 20-DEC-2001;

3 SHINTANI, NOBUTUHI MIYAJIMA

OS HOMO sapiens (human)

PN WO 0196567-A/1

PP 14-UTM-2001 WO 2001JP005061

PP 14-UTM-2000 JP 00P 184596,19-UUL-2000 JP 00P 223887 PI

TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC

C12M15/12 C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC

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WO 0196567-A/1.
Homo sapiens (human)
Homo sapiens
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AUTHORS
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Db 601 GTCTTCATCATTATGTTGATGGTGCAGCTACGCCACTCTTACTATCCCACGAGG 660  Cy 221 PhetrpalaglileulysAsmieuPhefileGlyValileLeuValCysPheleuPro 240  bb 661 TTCTGGGCTCAGCTGAAAACCTATTTTTTATAGGGGTCATCCTTGTTTCTTTC	SULT 2 498180 CUS FINITION Sequence 3 from Pate CESSION AX498180 I GI:23343 YHORDS Homo sapiens (human) ORGANISM Homo sapiens EUKARYOCA; HORAZOA; HOMMANIA; EUKHRYOCA; HORAZOA; HOMMANIA; EUKHRYOCA; HORAZOA; HOMMANIA; EUKHRYOCA; HORAZOA; HOMMANIA; EUKHRZIL, D TITLE TECEPTORE ATTENT FARENCE LICAL JOURNAL ATENT PATENT FARENCE LICAL ATURES LOCATION/OU SOURCE //OSGANISME // AMOLEYPE // AMOLEYP	Alignment Scores:  1.02e-110
AX481576 AX481576 AX481576 DNA linear PAT 16-AUG-2002 DEFINITION Sequence 1 from Patent EP1225183. ACCESSION AX481576.1 GI:22316490 KENYONDS SOURCE: Home sapiens (human) ORGANISM Harland.  REFERENCE 1 AMMERIA GIOTE HUMAN GIOTE STIME STATEM IN HOMINIGAE; Homo. AUTHORS HARLANd.  TITLE HUMAN GIOTE HUMAN GIOTE HUMAN GIOTE STATURES  LOCATION/QUALIFIERS  1. 918 DNA 116-AUG-2002  REFERENCE 1 AUTHORS AUTHORS 1. 918 DOUG 1:22316490  REFERENCE 1 AUTHORS BULKARYOTH HOMINIGAE; HOMO.  TITLE HUMAN GIOTE HUMAN GIOTE HOMINIGAE  JOURNAL PATENT IN HER GIORN PATENT IN C. (US) FEATURES  LOCATION/QUALIFIERS  1. 918 AUTHORS AUTHORS  LOCATION/QUALIFIERS  1. 918 AUTHORS AVA81576 AVA81576 AUTHORS AVA81576 AVA81576 AUTHORS AVA81576 AUTH	Alignment Scores:  1.02e-110	181 GTCCACAGGGTTTTTCTGCTGACAGGTGCCATTTCGCTTGACCTCATCAGAGACT  81 TrpMet PhedlyLeuProPheCyglysPheValSerAlaMetLeuHisIleHisMetTyr  84 TrpMet PhedlyLeuProPheCyglysPheValSerAlaMetLeuHisIleHisMetTyr  85 TrpMet PhedlyLeuProPheCyglysPheValSerAlaMetLeuHisIleHisMetTyr  86 TrpMet PhedlyLeuProPheCyglysPheValSerAlaMetLeuHisPhePheLygry  87 TrpMet PhedlyLeuPheTyrActyrSPheLyglyLeuHisPhePheLygry  88 TrpMet Tr

Run

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-MODEL=frame+ p2n.model-'DEV=xlh
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-UNITS=bits -START=1 -END=-1 -NATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-UNITS=bits -SOON -THE SCORE=50 - MILL SCORE=00000000
-USER=US10055106 @CGN 1 1 3508 @runat_21042004 161131_26182 -NCPU=6 -ICPU=3
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                                                                                         April 25, 2004, 18:51:16; Search time 4425 Seconds (without alignments) 2987.486 Million cell updates/sec
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1 MPGHNISRNSSCDPIVTPHL......GGSHWFKQKIIGLWNCVLCR
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                 nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Gallus ga Takifugu Zebrafish Zebrafish

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Homo sapi Sequence

AX498180 Sequence BD105324 Novel G I BD187510 Novel Pol AX481576 Sequence

Mon Apr 26 12:47:10 2004

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10S CATTTCCATTCTTTTCCTCC 124

Search completed: April 25, 2004, 18:51:08 Job time : 2953 secs

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contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-921
Fax: Authoric, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
Highh-efficiency full-length CDNA cloning. Methods Bnzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                  AUTHORS
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Eu (Dasse I to 686)

RS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building (1997)

AL Unpublished (1997)

Other GSSs: RPCI-11-229B2.TV

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

Research Genet cs (infc@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6

Class: BAC ends.
                                                                                                                                                                AQ488559 GSS 24-APR-1999 TRCI-11-229B2,TJ RPCI-11 Homo sapiens genomic clone RPCI-11-229B2,
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cDNA clone 5730578D17 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. 20;
iive 0; Mismatches 0; Indels
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1. .686
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clone="RPCI-11-229B2"
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                                                                    118 AAGACAAAGTGGAATTCTACA 138
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Mus musculus
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338 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 372g04, forward sequence, genomic survey sequence.
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE0927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Bmail: nelsaye@delgr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                      /moi_type="genomic_DNA"
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/note="vector: pBACe3.6; Site_1: EcoRI; Source DNA: Aedes
aegypti; strain unknown [derived from freshly hatched
larvae at the Virus Research Centre, Poona, India.
Reference: SINGH, K. R. P., 1967 Cell cultures derived
from larvae of Aedes albopictus (Skuse) and Aedes aegypti
(L.). Current Science 36: 506-508]; ATC-10 cell line ATCC
CCL-125"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

1 (bases 1 to 338)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hir Cambridge CBIO 18A, E-mail: barrell@sanger.ac.uk and mil@sanger.ac.uk
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100.0%; Pred. No. 17;
iive 0; Mismatches 0; Indels
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1. :501
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Class: BAC ends.
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Unpublished (2002)
Contract: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 405
Fax: 250 472 4075
Email: bkoopwive.c.
Email: bkoopwive.c.
Genome Sciences Centre, BC Cancer Agency
CDNA preparation, sequencing and bioinformatics:
Y Butterfield, R Kirkpatrick, J Asano, N Girn, R Guin, D Lee,
Y Butterfield, R Kirkpatrick, J Asano, N Girn, R Guin, D Lee,
S Lee, T Olson, P Pandoh, A Prahbu, D Smailus, L Spence, J Stott,
S Taylor, G Yang, J Schein, S Jones and M Marra.
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/ Organism="Salmo salar"
/ mol_type="mmkna"
/ mol_type="mmkna"
/ strain="McConnell"
/ db xref="texon:8030"
/ clone_lib="mixed_tisgue"
/ note="Vector: pcMvsport6; Library Creator: Research
/ note="vector: pcMvsport6; Usearch
/ simpn Jones (BS) Manaimo, B.C.), Seaspring Hatchery
(Crofton, B.C.), Rachel Roper (University of Victoria)"
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Email: enta@tigr.org
Library was provided by Susan Brown and Dennis Knudson at Colorado
                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostel, Euteleostei, Protacanthopterygii, Salmoniformes, Salmonidae, Salmo.

(bases 1 to 733)
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
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                                                                                                                                                                                GRASP Consortium, Davidson, W.S., Koop, B.F. and
http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
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Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D. Ends sequencing of Aedes aegypti BACs
Unpublished (2003)
Other_GSSs: CSU-K34 117019.T7
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100.0%; Pred. No. 0.042;
cive 0; Mismatches 0; Indels
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Pel: 301-838-3543
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Aedes aegypti
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                         Salmo salar (Atlantic salmon)
Salmo salar
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CC093858.1 GI:29954652
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Best Local Similarity 100.
Matches 26; Conservative
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Tel (bases 1 to 580)

Akinret, B., Levins, M., Mcgann, S., Taegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-211E13.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200
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                                                                                           /db_xref="taxon:10090"
/clone="INAGE:1988230"
/tissue type="spontaneous tumor, metastatic to mammary.
Stem ceIl origin."
Alab host="DH108"
/clone lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: lung vector: pCMV-SPORT6; Site_1: Sall;
/note="Torgan: lung vector: pcmv-vector: pcmv-vect
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Piecer de Jong
(pieter@dejong.med.bufalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 21 row: E column: 13
Seq primer: T7
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
bcorl; Site_2: BcoRi; Female C57BL/6J mouse kidney and/or
brain genomic DN was isolated and partially digested
with a combination of EcoRi and EcoRi Methylase. Size
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organism="Mus musculus"
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/clone="RPCI-23-211E13"
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/strain="C57BL/6J"
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                             mol_type="mRNA"
strain="Czech II"
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|lab_host="DH10B"
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selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CB514250 648 bp mRNA linear EST 16-MAY-2003 ssalrgb548309 mixed_tissue Salmo salar CDNA, mRNA sequence.
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/db_xref="taxon:8030"
/clone lib="mixed tissue"
/note="Wector: pdfWsport6; Library Creator: Research
Genetics; Atlantic salmon tissue contributors: Carlo
Bagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),
Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery
(Crofton, B.C.), Rachel Roper (University of Victoria)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRASP Consortium, Davidson, W.S., Koop, B.F. and
http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
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ssalrgb520231 mixed_tissue Salmo salar cDNA, mRNA sequence.
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                                                                                                                                                          ch 2.8%; Score 26; DB 28; Length 580; 1 Similarity 100.0%; Pred. No. 0.04; 26; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.041;
/ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Contract: Koop BF
Contract for Blomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3NS, Canada
Tel: 250 472 4075
Fax: 250 472 4075
                                                                                                                                                                                                                                                                                       643 TIACTATCCCACCAGGAGTTCTGGGC 668
                                                                                                                                                                                                                                                                                                                                   257 TTACTATCCCACCAGGAGTTCTGGGC 282

    648
    /organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"

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(bases 1 to 646)
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BF160725
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12 (bases 1 to 575)
13 Labass 1 to 575)
14 (bases 1 to 575)
15 Labo, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.

15 Use of EadC End Sequences from CalTech Libraries for Sequence-Ready Map Building

16 ther Gass: CITHEL-2569812.TR

17 Contact: Shaying Zhao, William Nierman, Mark Adams

18 Department of Eukaryotic Genomics

18 The Institute for Genomic Research

19 712 Medical Center Dr., Rockville, MD 20850

17 Tel: 301 838 0200

18 Fax: 301 838 0200

18 Email: hbe@tigr.org

18 Clones are available from Research Genetics (info@resgen.com). BAC ends search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

18 Seq primer: M13-21

18 Class: BAC ends.
                                                                                                                                                                                        AQ425698 575 bp DNA linear GSS 24-MAR-1999 CITBI-E1-2569B12.TF CITBI-E1 Homo sapiens genomic clone 2569B12, genomic survey sequence.
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0227962011 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/clone_lib="CITREL-B1"
/clone="Vector: pBeloBACil; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
                      Gaps
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3.2%; Score 29; DB 28; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 29; Conservative 0; Mismatches 0; Indels
                      Indels
                                                                                               143 Arcciaradreacececaciraarcaecereracricaras 184
                                                          79
                                                            38 ATCCIATAGIGACACCCCACTIAATCAGCCTCTACTICATAG
Best Local Similarity 100.0%; Pred. No. 1.1e-10; Matches 42; Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2569B12"
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AQ425698.1 GI:4495786
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Homo sapiens
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AQ425698/c
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BG862323
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Gaps ., 0 195

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BG461295 649 bp mRNA linear EST 21-APR-2001
RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG461295
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(Dases 1 to 649)

Harrington, U.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,

Manis, S., Leventhal, C., Thornton, M., Ramachandran, R.,

Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Greation of gene expression

activation of gene expression
/mol_type="mRNA"
/db xref="texcn:9606"
/cell line="HT1080"
/clone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/note="See" Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/clone="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression,
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 148; Conservative 0; Mismatches 0;
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3201 Carnegie Ave, Cleveland, OH 44115,
1212 16 431 9900
Fax: 216 361 9596
Email: scain@athersys.com.
Location/Qualifiers
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21227151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 crecregreadandacacecegrede 283
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/db_xref="taxon:9606"
/cell_line="HTT100"
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Eukaryota, Merazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 283)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Lerner,L., Costanzo,D., McBligott,K.,
Mhittington,J., Lerner,L., Costanzo,D., McBligott,K.,
Engenbacher,J., Danzig,J. and Ducar,M.
Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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RST41554 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG221739
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                                                                                                                                                                                                                                                    /organism="Homo sapiens"
//mol type="matkkk"
//db xref="taxon:9606"
/tissue type="normal nasopharynx"
/clone lib="human nasopharynx"
/note="ESTS generated from a normal nasopharynx cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  Transcriptional Gene Expression Profile of Human Nasopharynx
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                                                                                         Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
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/organism="Homo sapiens"
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Location/Qualifiers
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                        Unpublished (2003)
Contact: YiXin Zeng
Cancer Center
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BG221739
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Contact: Mahairas GG, Wallace JC, Hood L
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
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701 Fax: (206) 616-3887
8mail: jwallace@u washington.edu
701 Seattle: Jace@u washington.edu
701 Seatuen: http://www.htsc.washington.edu
702 Row: D column: 1
703 Plate: 3162 row: D column: 1
703 Seq primer: MI3 Reverse
704 Row: D column: 1
705 Seq primer: MI3 Reverse
706 Row: D column: 1
707 Row: D column: 1
708 Row: D column: 1
708 Row: D column: 1
709 Row: D column: 1
7
               1 (bases 1 to 456)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD699779 499 bp mRNA linear EST 25-JUN-2003 EST16303 human nasopharynx Homo sapiens CDNA, mRNA sequence. CD699779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GIGGIACCCCIGGIIGICICCCGGIAIGGAAICCAIGAGGAAIACAAIGAGGAGCACIGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 TTTAAATTTCACAAAGAGCTTGCTTACACATATGTGAAAATCATCAACTATATGATAGTC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 ATTITIGICATAGCCGITGCTGTGATTCTGTTGGTCTTCCAGGTCTTCATCATTATGTTG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ATINITIGICATAGCCGITGCIGIGATICIGITGGICTICCAGGICTICATCATTATGTTG 240
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 499)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ATGGTGCAGAAGCTACGCCACTCTTACTATCCCACCAGGAGTTCTGGGCTCAGCTGA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 GTGGTACCCCTGGTTGTCTCCCGGTATGGAATCCATGAGGAATACAATGAGGAGCACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 TACAGAAAACTGCATGCTGTGGCTGCCAGTGCTGGCATGTGGACGCTGGTGATTGTCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 456;
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26.9%; Score 247; DB 28;
Best Local Similarity 99.7%; Pred. No. 1.7e-120;
Matches 297; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=3162_Col=1_Row=D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/organism="Homo sapiens"
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Location/Qualifiers
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end was generated during the R&D process and may have higher chance of clone tracking errors. PRIMERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 TIGATGGIGCAGAAGCTACGCCACTCTTTACTATCCCACCAGAGTTCTGGGCTCAGGG 324
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                      / organism="pan troglodytes"
/ organism="pan onic DNA"
/ mol_xref="taxon:9598"
/ clone="RP43-C07G22.TJ"
/ sex="mall type="lymphocytes"
/ clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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Location/Qualifiers
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EcoRI
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Matches 513,
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MG145972 684 bp DNA linear GSS 08-JAN-2002
Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey
sequence.
                                            BF160725 601769127
AZ554824 RPC1-23-2
AZ554824 RPC1-23-2
CAC050323 sealrgb54
CAC050323 sealrgb54
CAC050323 sealrgb54
CAC050323 sealrgb54
CAC050323 sealrgb55
CAC09365 CSCY-K34.1
AA309267 AA4010267
AA309267 AA4010267
AA309267 AA4010267
AA309267 AA4010269
BK652637 Arabidops
BK65263 AGENCOURT
BC714391 AGENCOURT
BC71636 AGENCOURT
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BC71
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Totoki,Y., Matanabe,H. and Sakaki,Y.
Direct Submitssion

Birect Submitssion

and Chemical Research (RIXEN), Genomic Sciences Center (GSC);

1-7-22 Submitro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zan Luguruyres
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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BAC end sequences of Library RPCI-43
Unpublished
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                 AQ425698
BG862323
BF160725
AZ554824
CD514250
CA050323
CC093858
TA372G04P
                                                                                                                                                                                                                                    CB038895
BY186701
BE292324
CC873862
BZ863698
BZ349419
BU3419419
BU3628512
BU562963
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AK037644
CB118082
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AL762328
BX652637
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BU848450
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Pan troglodytes
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Result No.

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1 24885: contig of 24885 bp in length 4886 24985: gap of unknown length 4986 66573: contig of 41588 bp in length 6674 66673: gap of unknown length 10-cation/Qualiflers 1 .164055: contig of 97382 bp in length. 1 .164055 in troglodytes" | /mol type="genomic DNA" | /mol type="genomic DNA" | /db_Xref="taxon:9598" | /chromosome="UNK" | /chromosome="UNK" | /clone="RP43-126C6"
                                                                                                                                                                                                      1. .24885
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66674. .164055
/note="assembly_name:Contig5"
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Matches 887; Conservative
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δ	781	781 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG 840
q	15341	15341 AAGGITGCATTITATAACGAAATCTICTIGAGTGTAACAGCAATTAGCTGCTATGTTG 15282
ò	841	841 CTTCTCTTTGTCTTTGGGGAAGCCATTGGTTTAAGCAAAAAGATAATTG 889
qq	15281	15281 CTTCTCTTTGTGGGGGAAGCCATTGGTTTAAGCAAAGATAATTG 15233
Search	complet	Search completed: April 25, 2004, 19:56:46

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AC146385

Pan troglodytes chromosome UNK clone RP43-126C6, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. [ (bases 1 to 164055)

    Variable 1. Co 19405)
    Wilson, R. K.
    Direct Submission
    Submittered (13-AUG-2003) Genetics, Genome Sequencing Center, 4444
    Forset Parkway, St. Louis, MO 63108, USA
    Chases I to 164055)

                                                                                                        PAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG
                                                                                                                                CITCICITIGECITIGEGGGGAAGCCAITGGITIAAGCAAAAGATAAITGGCITAIGGAAI
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TACCAGTICITIAGGATCIATIACTIGAATGITGIGACGCATICCAATGCCTGTAACAGC
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Submitted (04-NOV-2003) Genetics, Genome Sequencing Center,
Forest Park Parkway, St. Louis, MO 63108, USA
On Nov 4, 2003 this sequence version replaced gi:33620890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13, 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162265 bases at least Q40
Consensus quality: 162289 bases at least Q20
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The sequence of Pan troglodytes clone Unpublished
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Pan troglodytes (chimpanzee)
Pan troglodytes
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AC146385.2 GI:38154073
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FLFYVVILVTRYLIFFKCKDKVEFYRKLHAVAASAGWNTLAVIVVPLVVSRYGIHEE
PLFYVVILVTRYLIFFKCKDKVTRYNTINTNIVITFTANAVILLVFQVFIIMLMVVGKLRHSLLSH
OBFWAQLKNLFFIGGLVATTVTLAVTRYLNVTHSNACNSKVAFTNBIFLSVTAIS
CYDLLLFVFGGSHWFKQXIIGLWNCVLCR"
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Pred. No. 0;
0; Mismatches 1; Indels
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Deleersnijder,W., Blockx,H. and de Moor,L.
Human g-protein coupled receptor and uses thereof
Patent: WO 0244212-A 1 06-JUN-2002;
SOLVAY PHARMACEUTICALS B V (NL)
Location/Qualifiers
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Best Local Similarity 99.9%;
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81 ATCCCTGGCCACAATACCTCCACAATTCCTCTTTCCATCCTTTTC 120 61 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGCTGGTGGGTG
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AX453412
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and

Haugen, E.D.

REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS TITLE	JOURNAL	AUTHORS	TITLE JOURNAL	COMMENT											
y 61 ATCAGCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGGTG	11600	y 121 CTCCTGGTGAAAATGAACACCCGGTCAGTGACCACCATGGCGGTCATTAACTTGGTGGTG 180	y 181 GICCACAGCGITITICIGCIGACAGIGCCAITICGCTIGACCICAICAAGAAGACT 240	11720	y 241 TGGATGTTTGGGCTGCCCTTCTGCAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300	y 301 CTCACGTTCCTATTCTAIGGGGGATCCTGGTCACCAGATACCTCATCTTCTAGAGGGC 360	y 361 AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGTGGCTGCCCAGTGCTGGCATGTGG 420 	/ 421 ACGCTGGTGATTGTCATTGTGGTACCCCTGGTTGTCTCCCGGTATGGAATCCATGAGGAA 480	481 TACAATGAGGAGCACTGTTTTAAATTTCACAAGAGCTTGCTT	/ 541 ATCAACTAIAIGAIAGTCAITHITIGTCAIAGCCGTIGCTGIGAITCTGTIGGCTTCCAG 600	601 GTCTTCATCATTATGTTGATGGTGCAGAAGCTACGCCACTCTTTACTACTCCCACCAGGAG 660	/ 661 TICTGGGCTCAGCTGAAAACCTAITTITATAGGGGTCATCCTTGTTTGTTTGCTTCC 720	721 TACCAGITCTITAGGATCTATTACTTGAATGITGTGACGCATTCCAATGCCTGTAACAGC 780	781 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTG 840	, 841 CTTCTTTGCTTTGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 900 	/ 901 TGTGTTTTGTGCGTTAG 918 	
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5': mapping in progress 3': RP11-243E12 (UWGC:djs156) AC018634, 6468-bp overlap

Overlapping Sequences:

Sequencing vector: plasmid; X52228; 100% of reads Chemistry: Dye-terminator BT-amersham; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 217693 bases at least 040 consensus quality: 218145 bases at least 020 consensus quality: 218145 bases at least 020 insert size: 273875; 19.1% error; agarose-fp Insert size: 273875; 19.1% error; agarose-fp Quality coverage: 8.30x in Q20 bases; agarose-fp Quality coverage: 10.42x in Q20 bases; sum-of-contigs

Direct Submission
Submitted (26-JAN-2001) Genome Center, University of Washington, Submitted (26-JAN-2001) Genome Center, University of Washington, Jan 26, 2001 this sequence version replaced gi:10567930.

Center: University of Washington Genome Center Center Code: UMCO.

Web site: http://www.genome.washington.edu

Contact: uwgchtgs@u.washington.edu ------- Project Information Center project name: HaaChr7 Center clone name: RP11-605P22 (djs708)

---- Summary Statistics

Kaul,R., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E. Direct Submission
Submitted (04-0CT-2000) Genome Center, University of Washington, 3 (bases 1 to 218186)
Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Haugen,E.D. and

Olson, M.V.

Large-scale Mapping and Sequencing of Human Chromosome 7 Unpublished

Kaul,R.K., Zhou,Y., James,R.A., Raymond,C., Olson,M.V.

(bases 1 to 218186)

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Sequence Validation:
This sequence has been validated by Multiple Complete Digest
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
finagments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.
BglII
ECORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.
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PRI 26-JAN-2001

AC083865 218186 bp DNA linear PRI 26-JAN-: Homo sapiens chromosome 7 clone RP11-605P22, complete sequence. AC083865

AC083865.2 GI:12545315 sapiens (human)

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 12 AC083865 LOCUS Homo sapiens Homo sapiens

Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A 1007 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JP); Center for Advanced Science and Technology Incubation, Ltd.
(JP)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 02064789-A 81 22-AUG-2002;
PHARMACIA & UPJOHN COMPANY (US)
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/organ.sm="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Local Similarity 100.0%; Pred. No. 0;
les 918; Conservative 0; Mismatches
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Sequence 81 from Patent W002064789.
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Homo sapiens
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Sejlitz,T. and Huff,R.M.

Novel g protein-coupled receptors
Parent: WO 0155473-A B1 25-MAY-2001,
PHARMACIA & UBJOHN COMPANY (US)
Location/Qualifiers
1. 2525
//organism="Homo sapiens"
//mol type="unassigned DNA"
/db_xref="taxon:9606"
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Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
                                                                                        ATCAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG
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	Oy 481 TACAATGAGGACTGTTTTAAATTTCACAAAGACTTGCTTACACATATGGAAAATC 540	541		Qy 721 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC 780	1003	OY 841 CTTCTTTTTTTTTTTTTTTGGGGAAGCCATTTAACAAAAATAATTGCTTTATGGAAT 300	Db 1123 'G'G'T'TG'G'G'TTAG 1140 RESULT 8 AX709195 LOCUS AX709195 1460 bp DNA linear PAT 04-APR-2003	AX709195 AX709195.1 GI:29564789	_	KEFEKENCE 1 AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G., Kallick, D.A., Gandhi, A.R., Walia, N.K., Arvizu, C., Elliott, V.S., Hafalia, A.J., Rankumar, J., Pei, J.J., Tang, Y.T., Redky, R., Burford, N. Lu, D.A., Graul, R.C., Khan, P.A., Walsh, R.T., Ison, C.H.,	1,B.A., Yang,J., Lee	Incyte Ge	/mol_type="lines agreed DNA" /do_xref="taxon:9606" /do_xref="laxyn:9606" /noTe="Incyte ID No: 90012670CB1"	Query Match Query Match 100.0%; Score 918; DB 6; Length 1460; Best Local Similarity 100.0%; Pred. No. 0; Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 ATG	
0	F4	Oy 901 TGTGTTTGTGCGGTTAG 918	RESULT 7 AX709194 AX709194 AX709194 DOCUS DEFINITION Sequence 53 from Patent WO02063004, ACCESSION AX709194 AX709194.1 GI:29564788 XFRANDRA	SOURCE Homo sapiens (human) ORGANISM Homo sapiens ORGANISM SURARYOLA; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE 1 AUTHORS Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G., Kallick, D.A., Gandhi, A.R., Walia, N.K., Arvizu, C., Elliott, V.S., Hafalia, J.J., Ramkumar, J., Pel, J., Tang, Y.T., Yue, H., Reddy, R., Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,	ĄŢ	FEATURES LOCALION/QUALILIES  Source 1. :1340  /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="Incyte ID No: 90012586CB1"	Query Match 100.0%; Score 918; DB 6; Length 1340; Best Local Similarity 100.0%; Pred. No. 0; Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 60	Qy 61 ATCAGCCTCTACTTAGTGCTTATTGGCGGGCTGGTGGTGATTTCCATTCTTTC 120	Qy 121 CTCCTGGTGAAAATGAACCGGGTCAGTGACCACGAGGGGTCATTAACTTGGTGGTG 180	Oy 181 GTCCACAGGGTTTTTCTGCTGACAGTGCCATTTCGCTTGACCTACCT	Qy         241 TGGATGTTTGGGCTGCCCTTCTGCAAATTGTGAGTGCCATGCTGCACATGTAC 300           L	Oy 301 CTCACGTTCCTATTCTATGGGGAACTCCTGGTCACCAGATACCTCATCTTCTAGGTGC 360	OY 361 AAAGACAAAGTGGAATTCTACAGAAAACTGCATGTGGGCTGCCAGTGCTGGCATGTGG 420	Oy 421 ACGCTGGTGATTGTCGTTGTGGTGTCTCCCGGTATGGAATCCATGAGGAA 480

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   A., Yang, J., Lee
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Richardson, T.W., Griffin, J.A., Warren, B., Harland, L.
G-protein coupled receptors
Patent: WO 02063004-A 52 15-AUG-2002;
Incyte Genomics, Inc. (US)
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Bughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G.,
Kallick, D.A., Gandhi, A.R., Walia, N.K., Arvizu, C., Elliott, V.S.,
Hafalia, A.J., Ramkumar, J., Pei, J., Tang, Y.T., Yue, H., Reddy, R.,
Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
     ACGCTCCTCGTGATTGTCATTGTCCTTGCTTGTCTCCCCCGGTATGCAATCCATGAGGAA
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CYDLLLFVFGGSHWFKQKIIGLWNCVLCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-ARR-2003) Neuroscience, Unit of Pharmacology, Uppsala University, Box 593, Uppsala 75124, Sweden Location/Qualifiers
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Homo sapiens G protein-coupled receptor 141 (GPR141) mRNA, complete
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Fredriksson, R., Hoglund, P.J., Gloriam, D.E., Lagerstrom, M.C. and Schioth, H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Seven evolutionarily conserved human rhodopsin G protein-coupled receptors lacking close relatives FEBS Lett. 554 (3), 381-388 (2003)
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                                                                       CTICTCTTTGTCTTTGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT
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Fredriksson, R., Hoglund, P.J., Gloriam, D.E.I., Lagerstrom, M.C. Schioth, H.B.
Direct Submission
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Patent: JP 2003024082-A 1 28-JAN-2003;
Pfizer Limited (EP (GB) only), Pfizer Inc (EP except GB / US / JP)
OS Homo sapiens
PN JP 2003024082-A/1
PD 28-JAN-2003
PP 17-JAN-2001
PP 73-JAN-2001 GB 0101739.1
PI harland lee
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Best Local Similarity 100.0%; Pred. No. 0;
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/organism="Homo Bapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD187510.1. GI:32997249
BD187510.1. GI:329972408
BD2 20031024082-A/1.
Homo sapiens
BUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
BUKaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1. (bases 1 to 918)
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BD105324.1 GI:22650898
WO 0196567-A/1.
Homo sapiens (human)
Homo sapiens (human)
Bullosize, metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Eukaryota; Lto, T.; Shintani, Y. and Miyajima, N.
Novel G protein-coupled receptor protein and its DNA
Backent: WO 0196567-A, I 20-DEC-2001;
TAKEDA CHEMICAL INDUSTRIES IJD, TAKEO MORIYA, TAKASHI ITO, YASUSHI
SHINTANI, NOBUYUKI MIYAJIMA
OS Homo sapiens (human)
PP 14-JUN-2001 JP 00P 184596, 19-JUL-2000 JP 00P 223887 PI
PR 15-JUN-2000 JP 00P 184596, 19-JUL-2000 JP 00P 223887 PI
TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC
C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC
A61K38/00,
PC A61K38/00, A61K48/00, A61P1/00, A61P9/10, A61P9/00, A61P25/28, PC
A61K38/00, A61K48/00, A61P3/00, G11N33/50, G11N33/50, G11N33/50, CC
Novel G protein-coupled receptor protein and its DNA FH Key
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Novel G protein-coupled receptor protein and its DNA.
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                                                                                                GICTICATCATTATGITGATGGTGCAGAAGCIACGCCACICTITACIAICCCACCAGGAG
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7. cyganism="Hono sapiens"
7. it type="genomic DNA"
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Endogenous and non-endogenous versions of human g protein-coupled
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Fromo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0242461-A 3 30-MAY-2002;
Arena Pharmaceuticals, Inc. (US)
Location/Qualifiers
1. .918
//organism="Homo sapiens"
//mol_type="unassigned DNA"
//db_xref="taxon:9606"
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Sequence 3 from Patent W00242461.
AX498180
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TGTGTTTTGTGCCGTTAG 918
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/mol_type="unassigned DNA"
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SUMMARIES

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APPLICANT: DEFENSE, BRADLEY
APPLICANT: HUMES, DEFEREY
TITLE OF INVENTION: CDNAS ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: CDNAS ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: CDNAS ENCODING PROTEINS
CURRENT APPLICATION NUMBER: US/08/676,351C
CURRENT FILING DATE: 1996-09-12
EARLIER APPLICATION NUMBER: PCT/US95/00939
EARLIER FILING DATE: 1995-01-20
EARLIER FILING DATE: 1994-01-21
NUMBER OF SEQ ID NOS: 11
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 1
ENGTH: 2706
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Patent No. 6005072
GENERAL INFORMATION:
APPLICANT: EPPLER, C. Mark
APPLICANT: HULMES, Jeffrey D.
TITLE OF INVENTION: DONA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       Length 2706;
                                                                                                                                                                                                                           Score 59.8; DB 2; Length 2
Pred. No. 9e-08;
0; Mismatches 297; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.6%;
Matches 251; Conservative (
                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
TISSUE TYPE: Rat brain
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STRANDEDNESS:
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                                                                                                                                ;
US-08-454-549-1
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6.5%; Score 59.8; DB 3; Length 2'
Best Local Similarity 45.6%; Pred: No. 9e-08;
Matches 251; Conservative 0; Mismatches 297; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,552
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RObinson, Joseph R.
REGISTRATION NUMBER: 0646/1A818-US4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (212) 753-6237
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US-08-676-351-1
; Sequence 1, Application US/08676351C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid
STRANDEDNESS: aingle
TOPOLOGY: linear
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ORIGINAL SOURCE:
; TISSUE TYPE: Rat brain
US-08-454-552-1
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                   366 CAAAGTGGAATTCTACAGAAAACTGCATGCTGTGGCTGCCAGTGCTGGCATGTGGACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: EPPLER, C. Mark
APPLICANT: OZENEBER, Bradley A.
APPLICANT: OZENEBER, Jeffrey D.
TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
TITLE OF INVENTION: TO OPIOID RECEPTORS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEB: Darby, & Darby, P.C.
STREET: New York
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,549
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RODINSON, JOSEPH R.
REGISTRATION NUMBER: 33,448
RESTRENCE/COCKET UNMBER: 064
TELECHMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
IENGTH: 2706 base pairs
TYPE: nucleic acid
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APPLICANT: Pasternak, Gavril W
APPLICANT: Pasternak, Mub USES THEREOF
TILLE REFERENCE: 830002-2004
CURRENT APPLICATION NUMBER: US/08/986,209A
CURRENT APPLICATION NUMBER: 1997-12-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Version 3.1
SEQ ID NO 1
LENGTH: 2600
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Query Match
6.5%; Score 59.8; DB 4; Length 2600;
Best Local Similarity 44.8%; Pred. No. 9.8e-08;
Matches 272; Conservative 0; Mismatches 332; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08986209A Patent No. 6660496 GENERAL INFORMATION:
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; LOCATION: (299)..(1402)
; OTHER INFORMATION:
US-08-986-209A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
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690 CCCTGGCTTCAGTGGTTGGTTCCTGTTGCCATCATGGGTTCAGCACAAGTGGAAGATG 749
                                                                                        750 AAGAGATCGAGTGCCTGGTGGAGATCCCTGCCCCTCAGGACTATTGGGGCCCTGTATTCG 809
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                                               65 GCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGG---TGTCATTTCCATTCTTTTCC
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45.6%; Pred. No. 6.6e-08;
tive 0; Mismatches 297; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER, READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: CONCURRENTLY herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATNOID, White & Durkee
STREET: P. O. Box 4433
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APPLICATION NUMBER: 08/120.601
PILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37,259
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REFERENCE/DOCKET NUMBER: IN
TELECOMMUNICATION INFORMATION
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 45.6
Matches 251; Conservative
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STATE: Texa
COUNTRY: US
ZIP: 77210
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                                                                       Mu Opioid Receptors: Compostions and Methods
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Pred. No. 6.6e-08;
0; Mismatches 297; Indels 3
                                                                                                                                                                                                      STALE..
COUNTRY: USA
ZIP: 77210-4433
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: PACHTIN Release #1.0, Version #1.25
``""WARE: PatentIN Release #1.0, Version #1.25
'`"""URARE: PatentIN Release #1.0, Version #1.25
'`"""URARE: PatentIN Release #1.0, Version #1.25
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                                                                                                                                      ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 CITY: Houston
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA
TELECOMMUNICATION INFORMATION:
TELEPAK: 512-418-3000
TELEPAK: 512-474-757
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 45.6%;
Matches 251; Conservative
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                          GENERAL INFORMATION:
APPLICANT: YL, Lei
TITLE OF INVENTION: Mu C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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EDNESS: single
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US-08-889-108-16
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RESULT 10
US-08-889-108-16
; Sequence 16, Application US/08889108
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Sequence 5, Application US/08292694A

Patent No. 6316686

GENERAL INFORMATION:
APPLICANT: BEILL, GRAENE
APPLICANT: YASUNA, KAZUKI
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P. O. Box 4433
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,694A
FILING DATE: AUGUST 19, 1994
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FILING DATE: 5 No. 6319686ember 1993
CLASSIFICATION 435
APPLICATION NUMBER: PCT/US94/05747
FILING DATE: 20 May 1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,296
FILING DATE: 20 May 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/100,694 FILING DATE: 30 July, 1993 CLASSIFICATION: 435
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ZIP: 77210
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US-08-292-694A-5
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STATE:
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                                                  REFERENCE/DOCKET NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:140/WIM
TELECOMMUNICATION INFORMATION:
TELEFRAX: (713) 789-2679
TELEFRAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pairs
TENGTH: 1330 base pairs
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 44.8%;
Matches 272; Conservative
           INFORMATION:
ATTORNEY/AGENT INFORMATI
NAME: MARK B. WILSON
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
161..1261
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; LOCATION:
US-08-292-694A-5
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Pred. No. 2.4e-08;
0; Mismatches 435; Indels
NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPROMENICATION INPORMATION:
TELEPRONE: (650) 845-4166
INPORMATION FOR SEQ ID NO: 1417:
SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         6.6%;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 44.24
Matches 351; Conservative
                                                                                                                                                                                                                                                                                              ; LIBRARY: GENBANK
; CLONE: 9532059
US-09-016-434-1417
                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                   TOPOLOGY: line
IMMEDIATE SOURCE:
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322 CTACTIGGCRGTGCATCGGGGGCTCCTGGGGAACTGCTCGTCGTGTATGTCATCCT 381
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FRILING DATE: 05-NOV-1993
CLASSIFICATION: 4315
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bell, Graeme I
APPLICANT: Reisine, Terry
APPLICANT: Yasuda, Kazuki
ITILE OF INVENTION: Opioid Receptor Genes,
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
AD
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APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION: 435
APPLICATION 435
APPLICATION: 435
APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     Sequence 5, Application US/08147592A
Patent No. 6096513
987 réaarcccarrerer 1001
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Best Local Similarity 44.8%;
Matches 272; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1330 base pair.
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LOCATION: 161..1261
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Sequence 1417, Application US/09016434

Patent No. 5500938

APPLICANT: USERRAL INFORMATION:
APPLICANT: Useffrey J. Sellhamer

TITLE OF INVENTION: ACMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS: 1490

CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE

CITY: PALO ALIO

STATE: CALIFORNIA

COUNTRY: USA
                Length 1177;
              Query Match 7.6%; Score 70.2; DB 4; Length 1
Best Local Similarity 46.6%; Pred. No. 4.1e-11;
Matches 225; Conservative 0; Mismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: HEREWITH
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                        ; DB 4; Length 1134;
5e-12;
                                                                                                                                                                                    Score 73.2; DB 4; Length 1
Pred. No. 5e-12;
0; Mismatches 263; Indels
PRIOR APPLICATION NUMBER: 60/093,002
PRIOR FILING DATE: 1996-07-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 1134
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                                                                                                                                                                                                                            Matches 231; Conservative
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; ORGANISM: homo sapiens
US-09-743-871B-13
                                                                                                              TYPE: DNA
CRGANISM: homo sapiens
US-09-743-871B-14
                                                                                                                                                                                                          Similarity
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US-09-743-871B-13
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8.3%; Score 76.4; DB 4;
Best Local Similarity 46.7%; Pred. No. 9.8e-13;
Matches 242; Conservative 0; Mismatches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 222181.1
US-09-976-594-171
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Sequence 14, Application US/09743871B
Patent No. 6627734;
GENERAL INFORMATION:
APPLICANT: Furness, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 cagggedecicación con contra decembro de contra de co
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     SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 GTTGCTGTGATTCTGTTGGTCTTCCAGGTCTTCATCAT 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1417:
SEQUENCE CHARACTERISTICS:
LENGTH: 1973 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; STRANDEDEES: SINGLE; TOPOLOGY: linear INMEDIATE SOURCE: LIBRARY: GENBANK ; CLONE: 9471316
                                                                                                                                                                       HEREWITH
                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Matches 242; Conser
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Sequence 171, Application US/09976594 Patent No. 6673549 GENERAL INFORMATION:

RESULT 4 US-09-976-594-171

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APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: IDENTIFICATION AND EXPRESSION OF MULTIPLE SPLICE VARIANTS OF MOUSI
TITLE OF INVENTION: KAPPA3-RELATED OPIOID RECEPTOR (KOR-3) GENE
FILE REFERENCE: 830002-2001.1
CURRENT APPLICATION NUMBER: US/09/743,871B
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: PCT/US/99/15977
PRIOR FILING DATE: 1997-07-15
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TILE REPRENEUE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PELL PROGRAM
SQ ID NO 171
LENGTH: 3205
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616 GATCGCTÁTGTAGCCATCTGCCACCCCÁTCCGTGCCTCCACCCÁCGTCCCAGCAAA 675
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                                                                                                                                                                                                                                                                                                                                                                            Length 1973;
                                                                                                                                                                                                                                                                                                                                                                            Similarity 46.7%; Pred. No. 7.4e-13;
42; Conservative 0; Mismatches 276; Indels
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APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Gocks, Benjamin G.
APPLICANT: Gocks, Benjamin G.
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: PALO ALTO
CITY: PALO ALTO
CITY: VALO ALTO
COUNTRY: USA
ZID: COLIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1417, Application US/09023655
Patent No. 6607879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati.
OPERATING SYSTEM: PC-DOS
                                                                 ; TYPE: nucleic acid
; STRANDENESS: single
; TOPOLOGY: linear
; INMEDIATE SOURCE:
; LIERARY: GENBANK
; CLONE: 9471316
US-09-016-434-1391
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-023-655-1417
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Best Local Simil
Matches 242; C
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        CIGGGGAACIGCCIIGICAIGIACGICAICCICAGGCACACAAAAIGAAGACAGCCACC 267
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                                                                                      ACCATGGCGGTCATTAACTTGGTGGTGGTCCACAGCGTTTTTCTGC
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patent No. 650038

GENERAL INFORMATION:
APPLICANT: Janica Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: PORPOSITION FOR THE DETECT:
TITLE OF INVENTION: COMPOSITION FOR THE DETECT:
TITLE OF INVENTION: PORPOSITION FOR THE DETECT:
TITLE OF INVENTION: AT 1900
CORRESPONDENCE ADDRESS: 1490
CORREST: 3174 PORTER PRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
ZIPU:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-055
TELEPRAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1391:
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APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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1480. Ap 11, Appl 3, Appli 3, Appli 3, Appli 9, Appli 1321, Ap 12, Appli 12, Appli 9, Appli

Run

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8.3%; Score 76.4; DB 4; Length 18
Best Local Similarity 46.7%; Pred. No. 7.1e-13;
Matches 242; Conservative 0; Mismatches 276; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: DC
CUMTARY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUW TYPE: FIDEPPY disk
COMPUTER: IBM PC COMPATIBLE
OFFRAMING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN RC-BOS/MS-DOS
SOFFWARE: PATENTIN RC-BOS/MS-DOS
SOFFWARE: PATENTIN RAPPLICATION DATA:
APPLICATION NUMBER: US/08/405,271A
FILING DATE: 14-MAR-1995
CLASSIFICATION: 435
ATTOMEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISCHATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 887-1500
TELEFAX: 90-4030 MRSNFORENSWSH
INPORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
          US-09-016-434-1480

US-08-147-592A-11

US-08-053-664A-11

US-09-472-130A-3

US-09-472-130A-3

US-09-472-130A-3

US-09-472-130A-3

US-09-472-130A-3

US-09-472-130A-3

US-09-473-871B-12

US-09-743-871B-12

US-09-174-43-871B-13
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                                                                                                                                                                                                                                                                                                                                                                                                US-081405-271A-18

Sequence 18, Application US/08405271A
Sequence 18, Application US/08405271A
SERERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: WORRISON & FORESTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, SU:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENES
                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1805 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
CDS
10..1119
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US-08-405-271A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: W
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Sequence 131, App
Sequence 171, App
Sequence 17, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 5, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appli
Sequence 11, Appli
Sequence 1, Appli
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5598.296 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                    April 25, 2004, 15:18:39 ; Search time
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Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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918
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94 CTGGTGGGTGTCATTTCCATTCTTTTCCTCCTGGTGAAAATGAACACCCGGTCAGTGACC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 GATCGCTATGTAGCCATCTGCCATCCGTGCCCTCGACGTCCGCAGCAAA 507
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8.3%; Score 76.4; DB 9; Length 1805;
Best Local Similarity 46.7%; Pred. No. 4.6e-12;
Matches 242; Conservative 0; Mismatches 276; Indels 0
                                                                                                                                                                                                                                                                              COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION NUMBER: 09/148,351
APPLICATION NUMBER: 09/148,351
FILING DATE: CDARIOWN-
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, RATE H.
REGISTRATION NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELERAM: (202) 887-0763
TELERAM: (202) 887-1500
TELERAM: (202) 887-1500
TELERAM: (202) 887-1050
TELERAM: (202) 887-1050
TELERAM: (202) 887-1050
TELERAM: (202) 887-0763
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: MORALSON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 10..1119
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-823-114-18
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LOCATION: 10.
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Db 628 CCTCAGGATTACTGGGGCCGGTGTTTGCCATCTTCCTTTCTTCTTCATCGTC 687

Oy S74 GTTGCTGTGATTCTTCGGGCCTGGTCTTCATCAT 611

Db 688 CCCGTGCTCGTCATCTTGTTGCTTGCTATGAT 725

Search completed: April 25, 2004, 17:54:03

Job time : 462 secs
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                                    APPLICANT: Unid, Peter
APPLICANT: Wood, Linds A.
APPLICANT: Parodi, Luis A.
TILE REFERENCE: 411USPHRM311 US/09/782,974C
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 06/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR PELICATION NUMBER: 06/165,838
PRIOR PELICATION NUMBER: 06/166,638
PRIOR PELICATION NUMBER: 06/166,071
PRIOR PELICATION NUMBER: 06/164,129
PRIOR PELICATION NUMBER: 06/184,129
PRIOR PELICATION NUMBER: 06/185,54
PRIOR PELICATION NUMBER: 06/185,54
PRIOR PELICATION NUMBER: 06/185,54
PRIOR PELICATION NUMBER: 06/186,530
PRIOR PELICATION NUMBER: 06/186,530
PRIOR APPLICATION NUMBER: 06/186,530
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NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
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Pred. No. 1.3e-108;
0; Mismatches 0;
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ilarity 99.8%;
Conservative 0
Publication No. US20030082534A1
GENERAL INFORMATION:
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US-09-782-974C-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 401; Conserv
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RESULT 14

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Sequence 540, Application US/09826509

| Sequence 540, Application US/09826509
| Publication No. US20030204073A1
| SEMERAL INFORMATION:
| APPLICANT: Lehmann-Eurinsma, Karin
| APPLICANT: Liaw, Chen W. |
| TITLE OF INVENTION: Protein-Coupled Receptors
| FILE REFERENCE: APPLICATION NUMBER: 06/195,747
| PRIOR APPLICATION NUMBER: 06/195,747
| PRIOR FILING DATE: 1998-10-13
| NUMBER OF SEQ ID NOS: 589
| SOFTWARE: PatentIN Version 2.1
| SEQ ID NO 540
| LENGTH: 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 ATTGCCATTGACTACTACATGTTCACCAGCACCTTCACCCTAACTGCCATGAGTGTG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 ACCAGATACCTCATCTTCTAGGAAGACAAAGTGGAATTCTACAGAAAACTGCAT 393
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Pred. No. 3.3e-12;
0; Mismatches 276; Indels
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KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
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Patent No. US20020061554A1
GENERAL INFORMATION:
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Best Local Similarity 46.7%;
Matches 242; Conservative
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CORGANISM: Homo sapiens
US-09-826-509-540
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US-09-782-974C-21/c
; Sequence 21, Application US/09782974C
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                      Query Match 61.1%;
Best Local Similarity 81.1%;
Matches 652; Conservative
                                                                                                                                                                                                TYPE: DNA
CORGANISM: Mus musculus
US-10-366-504-1
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Sequence 1, Application US/1036608A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Eishingdrelo, Haifeng
APPLICANT: Cai, Jidong
APPLICANT: Cai, Jidong
APPLICANT: Wright, Paul
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A G-PROTEIN-COUPLED RECEPTOR, AND UFILE REPERENCE: USAV2002/002 USNP
CURRENT APPLICATION NUMBER: US/10/366,504
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US 60/356,686
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: GB 0219574.1
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99.5%; Score 913.4; DB 15;
Best Local Similarity 99.9%; Pred. No. 7.2e-269;
Matches 914; Conservative 0; Mismatches 1;
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APPLICANT: GLUCKSNANN, MARIA ALEXANDRA; TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLE; TITLE OF INVENTION: RECEPTOR AND USES THEREFOR TILE REFRENCE: MD12001-021PARCPIN CURRENT FILING DATE: 2002-02-28; PRIOR APPLICATION NUMBER: US/10/085,233B; PRIOR FILING DATE: 2001-03-01; NUMBER: OF SEQ ID NOS: 6; SOTWARE: FaatSEQ for Windows Version 4.0; SEQ ID NO 3; LENGTH: 939
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ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: (1)
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US-10-085-233B-3
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99.8%; Score 916.4; DB 15; Length 1684;
Best Local Similarity 99.9%; Pred. No. 1.3e-269;
Matches 917; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10085233B

Publication No. US20030087249A1

Sequence 1, Application US/10085233B

Publication No. US20030087249A1

GENERAL INFORMATION

TITLE OF INVENTION: 93870, A HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTOR AND USES THEREFOR

FILE REFERENCE: MPI2001-021PIRCPIM

CURRENT FILING DATE: 2002-02-28

PRIOR PAPLICATION NUMBER: 05/10/085,233B

CURRENT FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PARESEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1684
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| LOCATION: (147)...(1085)
| COCATION: (147)...(1085)
| OTHER INFORMATION: n at position 1384 can be any
| OTHER INFORMATION: nucleotide
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ORGANISM: Homo sapiens
FEATURE:
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US-10-085-233B-1
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100.0%; Score 918; DB 16;
Best Local Similarity 100.0%; Pred. No. 7.1e-269;
Matches 918; Conservative 0; Mismatches 0;
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US-10-292-798-1007
| Sequence 1007, Application US/10292798
| Sequence 1007, Application US/10292798
| Publication No. US20030238933A1
| GENERAL INFORMATION:
| APPLICANT: SUMA, MAKIKO
| APPLICANT: ABLA, YUTAKA
| APPLICANT: ABLATANI, HIROYUKI
| TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
| FILE REFERENCE: 084335/166
| CURRENT PELICATION NUMBER: US/017,161
| PRIOR APPLICATION NUMBER: 10/017,161
| PRIOR APPLICATION NUMBER: 10/017,161
| PRIOR PILING DATE: 2001-06-18
| NUMBER OF SEQ ID NOS: 2070
| SOFTWARE: Patentin Ver: 2.1
| SEQ ID NO 1007
| LENGTH: 113306
| LENGTH: 113306
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ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
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Best Local Similarity 100.0%; Score 918; DB 10; Length 2525;
Best Local Similarity 100.0%; Pred. No. 5.5e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0;
                                                                                               901 TGTGTTTTGTGCCGTTAG
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CORGANISM: Homo sapiens
US-09-782-974C-81
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Best Local Similarity 100.0%; Pred. No. 3.5e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0;
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1193
LENGTH: 1318
                                                                                 TYPE: DNA CRGANISM: Homo sapiens FEATURE: NAME/KEY: SOURCE LOCATION: (1)..(1318) FEATURE:
                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (201)..(1118)
US-10-017-161-1193
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361 AAAGACAAACTGGAATTCTACAAAACTGCATGCTGGCTGG	RESULT 6  US-10-293-171-1  Sequence 1, Application US/10293171  Publication No. US20030138418A1  Sequence 1, Application US/10293171  Publication No. US20030138418A1  Sequence 1, Application No. US20030138418A1  APPLICANT: Cai, Jidong  APPLICANT:

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CICCIGGIGAAAAIGAACACCCCGGICAGIGACCACCACGATGCGCGCTCATIAACTIGGIGG 180
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721 TACCAGITCITTAGGATCTATTACTIGAATGITGIGACGCATTCCAATGCCTGTAACAGC
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Sequence 9, Application US/10188405

Publication No. US20030082585A1

GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT: Chen, Jin-Long

APPLICANT: Chen, Jin-Long

APPLICANT: Chen, Jin-Long

APPLICANT: Cutler, Gene

APPLICANT: Thiarik Inc.

ITLE REFERENCE: 0.18781-008410US

CURRENT FILING DATE: 2002-07-01

PRIOR FILING DATE: 2001-07-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9

LENGTH: 918

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LENGTH: 918

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LENGTH: 918
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100.0%; Score 918; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-270;
Matches 918; Conservative 0; Mismatches 0;
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COTHER INFORMATION: human TGR343

US-10-188-405-9
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ORGANISM: Homo sapiens
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US-10-188-405-9
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Sequence 1, Application US/10055106C
Publication No. US20030017536A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Fizer Inc.
APPLICANT: Harland, Lee
TITLE COF INVENTION: Novel Polypeptide
FIE REFERENCE: PC10970AGIK
CURRENT APPLICATION NUMBER: US/10/055,106C
CURRENT FILING DATE: 2002-01-23
PRIOR FILING DATE: 2001-01-3
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 918
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CORGANISM: Homo sapiens
US-10-055-106C-1
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o 17	3; Conservative 0; Mismatches 0; Indels 0; Gaps ArccrescocaaractecaegaartcTrargeGarcCTraraGTGACCCCACTA	Db 1 Argecraecacatacreeaeatacreeaearcerraecareeraraeraecacacacare 60 Oy 61 Arcaecaracaracaracaracacacacacacacacacaca				Db 241 1GGAIGTTIGGGCTGCCTTCTGCAAATTTGTGAGTGCCCATGCTGCACATGCTACC 300  OY 301 CTCACGTTCCTATGTGGTGATGCTGGTCAGTACCAGATACCTCATCTTCAAGTGC 360	Db 301 CTCACGTTCCTATGTGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC 360 Qy 361 AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGGCGGCTGCCAGTGCTGCTGGCATGTGG 420	Db 361 AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGTGGCTGCCAGGTGCTGCTGCTGGG 420  Qy 421 ACGCTGGTGATTGTGGTACCCCTGGTTGTCCCGGTATGGAATCCATGAGGA 480	421	Db 481 TACAATGAGGAGCACTGTTTTAAATTTCACAAAGAGCTTGCTT	Db 541 ATCACTATATGATGATCTTTTTTGTCGATGCCGTTGCTGTGATTCTGTTGGTCTTCCAG 600  Qy 601 GTCTTCATCATTATGTTGATGATGCTGCAGAGCTACGCCACTCTTTACTATCCAGCAGG 660  Db 601 GTCTTCATCATTATGTTGATGATGAAGAAGAAGCTACGCCACTCTTTACTATCCACCAGGAG 660	661 TICIGGGCTCAGCTGAAAACCTATTTTTATAGGGGTCATCCTTGTTTGT	OY 721 TACCAGTICTITAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC 780	OY 781 AAGGTTGCATTTTAPAACGAAATCTTCTGAGTGTAACAGCAATTAGCTGCTATGATTTG 840	OY 841 CTTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAGATAATTGGCTTATGGAAT 900  B41 CTTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 900	Oy 901 TGTGTTTTGTGCGTTAG 918  Db 901 TGTGTTTTGTGCCGTTAG 918	RESULT 4 US-10-055-106C-1
Oy 241 IGGAIGITIGGCCTCTCTGCAAATTTGTGAGTGCCATGCTGCACATGTAC 300  Db 241 IGGAIGTTTGGGCTGCCCTTCTGCAAATTTGTGAGTGCCATGCTGCACATGTAC 300	Qy 301 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCACATACCTCTTCTTCAAGTGC 360  Db 301 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACAGATACCTCATCTTCTAAGTGC 360	OY 361 AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGGGGGGGG	Oy 421 ACGCTGGTGATTGTCATTGTGGTACCCCTGGTTGTCTCCCGGTATGGAATCCATGAGGAA 480	Oy 481 TACAATGAGGAGCACTGTTTTAAATTTCACAAAGAGCTTGCTT	Qy 541 ATCAACTAIANGAIAGTCATTTTTGTCAIAGCCGTIGCTGTGAITCTGTTGGTCTTCCAG 600  541 ATCAACTAIATGAIAGTCAITTTGTCAIAGCCGTTGCTGTGAITCTGTTGGTCTTCCAG 600	OY 601 GICTICAICAITAIGHIGAIGAGAAAGCIACGCCACITIACIACIACCCACCAGGAG 660 	Oy 661 TTCTGGGCTCABAAAACTATTTTATAAGGGGTCATCCTTGTTTGTTTCCTTCC	Qy 721 TACCAGTTCTTTAGGAPCTATTACTTGAATGTTGTGACGCATTCCAATGCTGTAACAGC 780 Db 721 TACCAGTTCTTTAGGAPCTATTACTTGAATGTTGTGACGCATTCCAATGCTGTAACAGC 780	Oy 781 AAGGITGCAITITATAACGAAATCITCITGAGIGIAACAGCAAITAGCIGCIAIGAITIG 840 	Oy 841 CITCICITIGCIGAGGAAAGCCAITGGTITAAGCAAAAGAIAATIGGCITAIGGAAI 900 Db 841 CITCICITIGCTITGGGGAAGCCAITGGTITAAGCAAAAGAIAAITGGCTIAIGGAAI 900	Cy 901 TGTGTTTTGTGCGGTTAG 918 	RESULT 3 US-10-297-908A-2 ; Sequence 2, Application US/10297908A ; Publication No. US20040029793A1	GENERAL INFORMATION: APPLICANT: MORITY, Takeo APPLICANT: ITO, Takahashi APPLICANT: SHINTANI, Yasushi	, APPLICANT: MIXAJIMA, No. US20040029793Aluyuki ; TITLE OF INVENTION: No. US20040029793Alel G Protein-Coupled Receptor Protein and its ; FILE REPERENCE: 2737 USOP ; CURRENT APPLICATION NUMBER: US/10/297,908A	CURRENT FILING DATE: 2002-12-11 FRICK APPLICATION NUMBER: PCT/JP01/05061 FRICK FILING DATE: 2001-06-14 FRIOR APPLICATION NUMBER: JP 2000-184596	2225	; SEQ ID NO 2 ; LENGTH: 918 ; TYPE: DNA ; ORGANISM: Human

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PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 918
                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 918; Conservative
                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-995-225-3
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APPLICANT: Chen, Rucojing

APPLICANT: Chen, Rucojing

APPLICANT: Chen, Zhi Ling

APPLICANT: Chen, Zhi Ling

APPLICANT: Dang, Huong T.

APPLICANT: Dang, Huong T.

APPLICANT: Paritz, Kevin P.

BRING APPLICANTON NUMBER: US/09/2398

BRING APPLICANTON NUMBER: 60/253, 404

BRING APPLICANTON NUMBER: 60/253, 404

BRING APPLICANTON NUMBER: 60/202, 266

BRING BLING DATE: 2001-04-06

BRING PLING DATE: 2001-04-06

BRING BRING: APPLICANTON NUMBER: 60/290, 917

BRING BRING BRING: 67

BROWNERS PREACH NUMBER: 60/290, 917

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901 TGTGTTTTGTGCCGTTAG
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CRGANISM: Homo sapiens
US-09-995-225-3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 9, Appli	Sequence 1, Appli	119	Sequence 81, Appl	Sequence 1007, Ap	Sequence 1, Appli	Sequence 3, Appli	7	21,	Sequence 540, App
SUMMARIES	ΩI	US-09-995-225-3	US-09-995-225-3	US-10-297-908A-2	US-10-055-106C-1	US-10-188-405-9	US-10-293-171-1	US-10-017-161-1193	US-09-782-974C-81	US-10-292-798-1007	US-10-085-233B-1	US-10-085-233B-3	US-10-366-504-1	US-09-782-974C-21	US-09-826-509-540
	DB		10	13	13	15	15	15	10	16	15	15	15	10	11
	% Query Match Length DB	918	918	918	918	918	1040	1318	2525	113306	1684	939	810	447	1113
	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	8.66	99.5	61.1	42.5	8.3
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Sequence 18, Appl	Sequence 18, Appl	Sequence 9, Appli	Sequence 10, Appl	H	1391	Sequence 22, Appl	208,	31, 4	7, 7		13,	٠,	Sequence 1, Appli	• •	9, A	542,	21,	147,	19, 7	1417	19,	Seguence 14, Appl	1, 7	Sequence 3, Appli	3, A	e 15, A	171	278	Sequence 12, Appl	148
US-09-823-114-18	US-10-	US-09-	-60-SD	O US-09-905-186A-11		5 US-10-087-345A-22	US-10-2	5 US-10-352-684A-31	J US-09-905-186A-7	0 US-09-905-186A-8	US-10-087-	S US-10-029-386-9800	-506-60-SD	US-10-029-3	0 US-09-910-695-9	US-	US-10-345-	US-10-22	US-10-345-680	S US-10-305-720-1417	US-10-087-	음	5 US-10-318-661-1	5 US-10-318-661-3	US-09-170-919-3	US-10-251-38	5 US-10-251-385-171		3 US-10-433-561-12	S US-10-305-720-1480
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8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.3	8.1	8.1	7.8	7.7	7.6	6.9	6.8	9.9	9.9	9.9	9.9			6.5		6.5	6.3	6.3	•	6.3	6.3	6.3
76.4	76.4	76.4	76.4	76.4	76.4	76.4	76.4	76.4	74.8	74.8	71.6	70.4	9.69	63.4	62.8		61		19	61	<u>.</u>	59.8	σ	σ	ъ				28	
15	16	17	18	19	20	21	22	23	24	25	c 56	27	28	29	30	31	32	33	34	35	36	37	38	99	04	41	42	43	44	45

## ALIGNMENTS

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publication No. US2020193584A1
| Sequence 3, Application US/09995225
| Facquence 3, Application US/09995225
| Facquence 4, Application No. US2020193584A1
| GENERAL INFORMATION:
| APPLICANT: Chu, Zhi Liang
| TILLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
| TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
| TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
| TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
| TITLE OF INVENTION: Endogenous And No. US20021398
| PRIOR PLILNG DATE: 2000-11-26
| PRIOR PLILNG DATE: 2001-02-20
| PRIOR PLILNG DATE: 2001-02-20
| PRIOR PLILNG DATE: 2001-04-06
| PRIOR PLILNG DATE: 2001
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Enail: mmpratt@qqq edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; tissue and RNA were prepared in the Department of Large
Animal Medicine, University of Georgia; sequencing done in the
Laboratory for Genomics and Bioinformatics, University of Georgia.
Sequence ends have been trimmed to exclude vector and regions below
Phred quality 16. Three-prime sequences are presented as their
reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
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LeukoS2_2 H07.gl_A024 Stimulated peripheral blood leukocytes S2
Eguus caballus cDNA clone LeukoS2_2_H07_A024 S', mRNA sequence.
                                                                                                                                                                                                              /cell type="NOD-derived CD11c +ve dendritic cells"
/clone lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                          572
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 679)
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assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Unpublished (2003)
Other ESTS: LeukoS2_2 H07.bl_A024
Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fat: 706 542 1860
                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                             Score 83.6; DB 13; Length 661;
Pred. No. 1.4e-11;
0; Mismatches 34; Indels 1;
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                                                                                       1 . 661

Organism="Mus musculus"

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/strain="NOD"

/db_xref="taxon:10090"

/clone="F630103H01"
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/db_xref="taxon:9796"
                                                               Location/Qualifiers
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EST.
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illarity 76.7%;
Conservative (
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AUTHORS
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/cell_type="leukocytes"
/lab_host="Heukocytes"
/lab_host="Hilds Ti phage-resistant E. coli"
/lab_host="Hilds Ti phage-resistant E. coli"
/clone_lib="Stimulated peripheral blood leukocytes S2"
/note="Organ: circulatory system; Vector: pME185-FL3;
Site_1: Xho1; Site_2: Xho1; The library was prepared from poly4+ RNA from equine peripheral blood leukocytes simulated from a healthy adult horse. The leukocytes were stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.
Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME185-FL3 vector (5-prime Dialize is CACCATGTG', 3-prime DraIII site is CACCATGTG'.
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'clone="LeukoS2_2_H07_A024"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

musculus (house mouse)

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SOURCE
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                                                                              /clone lib="Carp mixed tissue library 2"
/note="Vector: pTriplEx2; Site 1: Sfil GGCCATTACGGCC;
Site= 2: Sfil GGCGCCTCGGCC; Normalized and serially
subtracted cDNA library prepared from mixed tissues of
warm, cold and hypoxia challenged animals"
                                                                                                                                                                                                                                                                                                                                                                                                                                  148 AGTCCCAAAGGCGTCTCTCTTTCACCAAAGTGTCTGTAATCAACCTGATAGCAGTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 TATTITCTGCTCAAAGTGAGTAAAACATTTGGAAAGGCCACATGTCAACGTCAAGAGTTC
                                                                                                                                                                                                                                                                      Gaps
/tissue_type="Skeletal white muscle, cardiac muscle, Addney, brain, gill, intestinal mucosa" /dev esege="Adult" /lab_host="E.coli Electromax DH108"
                                                                                                                                                                                                                        Score 104.4; DB 14; Length 844;
Pred. No. 3e-17;
0; Mismatches 322; Indels 10;
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Best Local Similarity 51..1
Matches 347; Conservative
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Contact: Yoshihide Hayashizaki

22354683

TITLE

Mikaido, I., Osato, N. Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, T., Osato, N., Satto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Sito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schrim, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Gasterland, T., Rawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Besole, J., Marchlonni, L., Mokenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Taylor, M.S., Taylor, M., Sandilin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Varagisawa, M., Yang, I., Yangteu, M., Hirozane-Kishikawa, T., Yangteu, M., Hirozane-Kishikawa, T., Yangteu, M., Hirozane-Kishikawa, T., Yangteu, M., Hirozane-Kishikawa, T., Waki, K., Kawai, J., Aizawa, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Haysahizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNa

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Laboratory for Genemican, Industriant Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Email: genome-resegneriken.go.jp,
URL:http://genome-gec.riken.go.jp,
URL:http://genome-gec.riken.go.jp,
URL:http://genome-gec.riken.go.jp,
Radchi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Habilzume,W., Hayashida,K., Hiozane,T., Hori,P.,
Imocani,K., Ishii,Y., Itch,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Supmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Computational Analysis of Full-Length Mouse CDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RIEA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
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EST 17-DEC-2002

BY748361 BIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus CDNA clone F630103H01 5', mENA

BY748361 BY748361.1 GI:27177122 EST.

ACCESSION VERSION KEYWORDS

sequence.

RESULT 14 BY748361 LOCUS DEFINITION

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Cyprinus carpio (common carp)

ISM Cyprinus carpio (common carp)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Meopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprinus.

Gyacey, Ar.; Fraser, E., Li, W. and Cossins, A.R.

Microarray and EST analysis of the carp (Cyprinus carpio)

transcriptome during environmental stress

Microarray and EST analysis of the carp (Cyprinus carpio)

transcriptome during environmental stress

Microarray of Environmental Gene Regulation

Unpublished (2003)

Contact: Andrew R. Cossins

Laboracory for Environmental Gene Regulation

University of Liverpool

School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 72B

Tel: +44(0)151-795-4431

Email: cossins@ilv.ac.uk

Vector has been trimmed from this EST.

Plate: 15 row: h column: 17

Seq primer: Triplex 5' LD (5'-CTCGGGAAGCGCCATTGTGTTGGT-3')

High quality sequence stop: 580.

Location/Qualifiers

// Contaction/Qualifiers

// Contaction/Qualifiers

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CCLXOSal5h17fl Carp mixed tissue library 2 Cyprinus carpio cDNA clone 15h17 5', mRNA sequence.
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                                                                                                                                                                                                                        110 CCATTCTTTTCCTCCTGGTGAAAATGAACACCCGGTCAGTGACCACCATGGCGGTCATTA
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                                                                                                                                             Gaps
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                                                              Length 680;
                                                                                                                                             Indels
                                                              Score 111; DB 14;
Pred. No. 4.3e-19;
0; Mismatches 166;
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                                                                      12.1%;
                                                                                                                                                      Matches 210; Conservative
                                                                                                                Similarity
                                                                           Query Match
Best Local 8
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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CA965628
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Oncorbynchus mykiss
Oncorbynchus mykiss
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi, Actinopterygii, Neopterygii, Teleostei; Euteleostei;
Protacanthopterygii, Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 680)
Sequence analysis of a rainbow trout normalized cDNA library Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             þ
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/note="Vector: pCWV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outputs. 1202. (2022.)
Contact: Record CE
Contact: Record CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Fax: 304 725 0351
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified b
cross_match v0.990329.
Seq primer: AGCGGATATTTCACACAGGA.
Location/Qualifiers
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                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                       Query Match
Best Local Similarity 64.1%; Pred. No. 1.5e-27;
Matches 225; Conservative 0; Mismatches 125; Indels
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/db_xref="taxon:8022"
/dev_stage="2-3 weeks old"
/clone lib="riken1"
/note="CB inbred strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IRT88K09 A F05"
/tissue_type="pooled"
/lab_host="DH108"
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1 (bases 1 to 834)

Bustrefedde, J. M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
                                                                                                                                                                                                                                                                                              663 AIGTGGCCATTGTTACCCTTCGGCTGCTCATCTATTAAG---AAACTGCAAATGCAAC
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AJ455645 rikenl Gallus gallus cDNA clone 6b4r1, mRNA sequence.
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Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 22, 20251 Hamburg, Germany
Emall: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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/cell_type="bursal lymphocyte"
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cDNA library was propered and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to Division visit on the search for further and sequenced in Riken contributed to Division with the search in Riken search in Riken contributed to Division with the search searc
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vgTvmAsshwmpkrncQsMlatiiniivlhsllislpprrsyypsavwklgsptcry
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IIFAYWPDWMAHQEYERQERFEFHKSLNSRDIIINVSIIVIMMTTVLLIFLIQMAVILH
BICVALTAPCCLDMLCFIGGVIH"
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
.dev_stage="adult"
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Pred. No. 1.7e-28;
0; Mismatches 373; Indels 12;
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(InterPro|IPR000276, evidence: InterPro)
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="MG1-2406345"
/db_xref="taxon:10090"
/clone="A530099J19"
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'protein_id="BAC30904.1"
'db_xref="GI:26334373"
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/strain="C57BL/6J"
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Rhodopsin-like GPCR superfamily containing protein, full insert
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2774)
                                                                                                                                                                                               136 Areccresceacaracerceassarrecrerressarcerarassascaceceaerra 195
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                              196 AICAGCCCTACTICATAGTGCTTATTGGCGGGCTGGTGGTGGTCATTTCCATTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
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    expressed in HT1080 under normal circumstances.
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                                                                                                             Indels
                                                                   Length
                                                                 ore 148; DB 12;
red. No. 2.1e-29;
Mismatches 0;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
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HTC, CAP trapper.
Mus musculus (house mouse)
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les 148; Conserv
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Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Lerner, L., Costanzo, D., McBlligott, R., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Gffenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random activation of gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG221739 283 bp mRNA linear EST 21-APR-2001
RST41554 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG221739
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/collline="HT1080"
/coloellib="Atherses RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Blotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                            41; Indels
                                                                                                                                                                                                                                              Score 151.4; DB 12;
Pred. No. 3.1e-30;
0; Mismatches 41; 1
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Fax: 216 361 9596
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/mol_type="mRNA"
/db xref="taxon:9606"
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Location/Qualifiers
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Athersys, Inc.
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ilarity 81.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 TIGACCIACCICATCAAGAAGACTIGGAIGITIGGGCIGCCCITCIGCAAAITIGIGAGI 276
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                                                                                                                                       38 ATCCTATAGIGACACCCCACTTAATCAGCCTCTACTTCATAGIGCTTATTGGCGGGCTGG
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             Pred. No. 3.8e-37;
                                                      0; Mismatches
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             Best Local Similarity 75.5
Matches 323; Conservative
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| /coll_line="HT1080" |
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1 (bases 1 to 649)
Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Mhittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mys, R., Sanith, B., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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/tissue lip="human nasopharynx"
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3201 Carnegle Ave, Cleveland, OH 44115, USA
TTE1: 216 431 9500
Fax: 216 361 9596
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                                                                                                                                                                                                                                                                                                                                          Query Match 20.6%; Score 189; DB 14; Best Local Similarity 100.0%; Pred. No. 1.6e-40; Matches 189; Conservative 0; Mismatches 0;
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Location/Qualifiers
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BG145683 478 bp mRNA linear EST 01-FEB-2001 mac33c07.y1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:4001652 5', mRNA sequence.
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Mus musculus
Mus musculus
Mus musculus
Mus musculus
Muscayous, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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High quality sequence stop: 392.
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/clone="IMAGE:4001652"
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Site 2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
and Differentiation 7, 3-11 (1996)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer Center
Sun Yat-sen University
Sin Nat-sen University
651 DongPeng Road Bast, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
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. .646
organism="Mus musculus"
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                                                                                                                                           /db xref="taxon:10090"
/clone="IMAGE:4917024"
                                                           /mol_type="mRNA"
/strain="NMRI"
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Contact: YiXin Zeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Contact: Robert Strausberg, Ph.D. Email: cgapba-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                   /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TACAGAAAACTGCATGTGGCTGCCAGTGCTGGCATGTGGCTGGTGATTGTCATT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10828 row: b column: 01
High quality sequence stop: 644.
Location/Qualifiers
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                               /orgānism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
|clone="plate=3162 Col=1 Row=D"
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

LOCUS DEFINITION

RESULT 5 BG862323

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end was generated during the R&D process and may have higher chance of clone tracking errors. PRIMERS
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                                                                                                                                                                                                                                                                              Gaps
                                                                                                                  1. .684
/organism="Pan troglodytes"
/mol_trog="genomic DNA"
/mol_trog="texton:9598"
/clone="RP43-007G22.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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                                                                                                                                                                                                                                                   684;
                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                   Length
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59.0%; Score 542; DB 29;
Best Local Similarity 98.2%; Pred. No. 3e-137;
Matches 548; Conservative 0; Mismatches 10;
                                                                 Vector : pBACe3.6
R.Site 1 : ECORI
R.Site 2 : ECORI.
Location/Qualifiers
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EST. Mus musculus (house mouse)

GI:11040832

BF160725.1

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Sases I to 772)

8 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Famali: Capabs-ramali.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
Email: Capabs-ramali.nih.gov

Tissue Procurement: Gilbert Schoologies, Inc.

Colne Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9196 row: f column: 07

High quality sequence stop: 634.

11.77.***

Location/Qualifiers

Juccontrol Column: 07

High quality Sequence stop: 634.
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/dlone="MAGE:3988230"
/folone="MAGE:3988230"
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/mol_type="mRNA"
/strain="Czech II"
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Matches 545; Conservative
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Louder, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Direct Submission
Direct Submission
Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, Withttp://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
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Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey
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(bases 1 to 684)
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Result No.

BC862223 602796201 BC669779 EST16303 BC461295 RST41634 BC461295 RST41634 BC45131739 RST41554 AC041317 Mus muscu AC055645 AJ45645 CA355790 627748 NC CA35790 BC748361 CA35790 BC748361 CA56527 LeutkoS2 2 CA050323 H4779D04-AV410745 Homo sapi BY36120 BY75012 BY1614184 AGENCOURT BY752012 BY75012 BY183952 BY750559 BY75172 BY750559 BY751732 BY751732 CD559646 AGENCOURT CD55964 AGENCOURT BE19833 BU77612. y AV400332 Homo sapi BM54614 AGENCOURT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel G-protein coupled receptor polypeptides referred as GCREC peptides, useful for treating multiple sclerosis, cholecystitis heart failure, angina pectoris, rheumatoid arthritis, obesity, osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human G-protein coupled receptor (GCREC 1-16) polypeptides and polynucleotides. Sequences of the invention are useful cor the diagnosis, treatment and prevention of cell proliferative (e.g. cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris, near failure), gastrointestinal (e.g. multiple sclerosis, cholecystitis), autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis) and metabolic disorders (e.g. obesity, osteoporosis), viral infections, atherosclerosis and hepatitis, GCREC proteins are useful for identifying compounds that modulate, mimic and block olfactory and taste sensations. They are also useful for identifying GCREC modulators. GCREC DNAs are useful in gene therapy. The present sequence is human GCREC-6 cDNA
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97.5%; Score 895; DB 6; Length 1499;
Best Local Similarity 99.9%; Pred. No. 3e-254;
Matches 906; Conservative 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1499 BP; 375 A; 340 C; 329 G; 455 T; 0 U; 0 Other;
                                                     Location/Qualifiers
381. 1400
/*tag= a
/product= "Human GCREC-6 protein"
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13-CCT-2000; 2000US-0240589F.

20-CCT-2000; 2000US-024323F.

20-CCT-2000; 2000US-024585F.

03-NOV-2000; 2000US-0245865F.

09-NOV-2000; 2000US-024580F.

15-NOV-2000; 2000US-024587F.
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Ramkumar J,
Elliott VS,
Nguyen DB, I
                 Homo sapiens
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CTCCTGGTGAAAATGAACACCCGGTCAGTGACCACCATGGCGGTCATTAACTTGGTGGTG
                                                                                           TGGATGTTTGGGCTGCCCTTCTGCAAATTGTGGGGGCGTGCGCTGCACATCCACATGTTAC
                                                CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTAAGTGC
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                          /*tag= a
/partial
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/ganduct= "Human G-protein coupled receptor type protein
93870"
                                                                                                                                                                                                                                                                                                                                                    New G-protein coupled receptor used in receptor assays as a target for disgnosis and treatment of receptor-mediated disorders, e.g. immune and inflammatory disorders, platelet disorders, skeletal or bone metabolism
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                                                                                         stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 101-103; 105pp; English.
                                                                                                                                                                                   28-FEB-2002; 2002WO-US006455
                                                                                                                                                                                                                  01-MAR-2001; 2001US-0272677P
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             1. .939
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P-PSDB; AAO22919.
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                                                                                                                                                                                                                                                                                Glucksmann MA;
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Human, G-protein coupled receptor-6; GCREC-6; atherosclerosis; cancer; cell proliferative disorder; gastrointestinal; autoimmune; metabolic; neurological; inflammatory; cardiovascular; viral infection; anorexia; cirrhosis; multiple sclerosis; Huntington's disease; gene therapy; Alzheimer's disease; heart failure; hepatitis; cholecystitis; obesity; rheumatoid arthritis; Hashimoto's thyroiditis; angina pectoris; osteoporosis; gene; ss.

disorders. 

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WPI: 2002-732793/79.
                                                           P-PSDB; AA022919
Glucksmann MA;
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New G-protein coupled receptor used in receptor assays as a target for diagnosis and treatment of receptor-mediated disorders, e.g. immune and inflammatory disorders, platelet disorders, skeletal or bone metabolism

Claim 5; Page 99-100; 105pp; English

The invention relates to an isolated polypeptide, which is a G-protein coupled receptor (GPCR) related to Subfamily I of G-protein coupled receptor (GPCR) related to Subfamily I of G-protein coupled receptor type proteins (GPCRs), designated the 93870 receptor. The polypeptides, nucleic acid molecules and antibodies of the invention are nother of the 93870 polypeptides or prediction (e.g. diagnostic assays, treatment (e.g. therapeutic and prophyladis), or in methods of treatment (e.g. therapeutic and prophyladis). They are useful in treatment (e.g. therapeutic and prophyladis or nucleic acids, e.g. immune and inflammatory disorders, platelet disorders, skeletal or bone metabolism disorders, or bone marrow mononuclear disorders, as well as cellular proliferative and/or differantiative disorders, viral as cellular and pain and metabolic disorders, viral diseases, liver disorders, and pain and metabolic disorders. Conditions that can be treated include cancer, diabetes mellitus, hypothyroidism, changed partial meningencephalitis, multiple sclerosis, hypothyroidism, reproductive or fertility disorders, HIV, bacterial or viral meningitis, fungal meningencephalitis, multiple sclerosis, Hutlangton's disease, astala-telangiectersia, the function, rheumatoid arthritis, dermatitis, garaft-versus-host inflammatory bowel disease, asthma, conjunctivitis, garaft-versus-host changease, allersy, idiopathic thrombocytopenia, or osteoporosis. The transgenic animals are useful for studying the function and/or activity of 93870 activities. The polymucleotide sequence represents the cDNA of the invention can be used in the study.

Sequence 1684 BP; 435 A; 366 C; 351 G; 531 T; 0 U; 1 Other;

120 CTCCTGGTGAAAATGAACACCCGGTCAGTGACCACCATGGCGGTCATTAACTTGGTGTG 350 240 410 360 530 290 CTCCTGGTGAAAATGAACACCCGGTCAGTGACCCACCATGGCGGTCATTAACTTGGTGGTG 180 TGGATGTTTGGGCTGCCCTTCTGCAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC 300 TGGATGITTGGGCTGCCCTTCTGCAAATTTGTGGGCGATGCTGCACATCCACATGTAC 470 AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGTGGCTGCCAGTGCTGGCATGTGG 420 60 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCGTCTTCTTCAAGTGC CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGGGTGTCATTTCCATTCTTTC Grecacacidririteracracidacacidentricaciridaceracereargaagaer 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA Gaps ; 0 Ouery Match

99.8%; Score 916.4; DB 6; Length 1684;
Best Local Similarity 99.9%; Pred. No. 1.4e-260;
Matches 917; Conservative 0; Mismatches 1; Indels 0; 171 231 121 291 351 411 61 181 241 301 471 ద δ 요 à 8 8 ద ठे g g Ś ò

780 950 840 900 770 999 830 720 890 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG GICTICATCATCATGATGATGGAGAAGCTACGCCACTCTTACTATCCCACCAGGAG **AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG** AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGTGGCTGCCAGTGCTGGCATGTGG Accordentation cantered as a contraction of the cont ATCAACTATATGATAGTCATTTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCCAG Arcaactatatgatagtcartritgtcaraccertecterereatreregererected TACCAGTICITITAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC raccagnicinnaganchantachrantanghanghangcachniccandcondracago GTCTTCATCATTATGTTGATGGTGCAGAAGCTACGCCACTTTTACTATCCCACCAGGAG 1071 rererrrrereceerrae 1088 918 rererrrrereccerrag 831 1011 531 421 591 651 541 711 771 661 891 781 951 841 901 481 601 721 8 6 8 6 6 6 ठ 8 & 8 ò 셤 ठे 원 셤 6 음 셤 ઠે

AAL53414 standard; DNA; 939 RESULT 14 AAL5341 

AAL53414;

ВЪ

(first entry) 12-DEC-2002

nt coding DNA of a human G-protein coupled receptor type protein.

KW Anti-HIV; cytostatic; antidiabetic; antiasthmatic; antiinflammatory; haemostatic; neuroprotective; nootropic; immunosuppressive; osteopathic; antibacterial; virucide; funglicide; analgesic; antipactrial GPCR; artibacterial; virucide; funglicide; analgesic; antiallergic; cardiant; dermatological; antiinfertility; hepatotropic; antiallergic; mantipamatic; ophthalmologial; antianginal; antithyroid; anticonvulsant; antipacmatic; ophthalmologial; antianginal; antithyroid; anticonvulsant; mantipsoriatic; antiarthritic; d-protein coupled receptor; subfamily I; kW antitheumatic; antiarthritic; d-protein coupled receptor; subfamily I; kW skeletal; bone metabolism disorder; bone marrow monouclear disorder; selectal; bone metabolic disorder; bone marrow monouclear disorder; neurological disorder; cardiovascular disorder; wiral disease; pain; liver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial; kW hypothyroidiam; hypothyroidiam; reproductive; fertility disorder; HIV; viral meningitis; fungal meningon-cephalitis; multiple sclerosis; mycardial infarction; rheumatoid arthritis; multiple sclerosis; mycardial infarction; rheumatoid arthritis; psoriasis; crohn; disease; antimatory bowel disease; asthan; saffiner disease; allergy; representation; animal; hyman; crons, dermandicial; hyman; crons, dermandicial; hyman; crons, dermandicial; hyman; crons, dermandicial; crons, allergy; representation; animal; hyman; crons, dermandicial; osteoporosis; gene therapy; transgenic animal; human; gene; ds.

sapiens

361

Location/Qualifiers

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660 GTCTTCATCATTATGTTGATGGTGCAGAAGCTACGCCACTCTTTACTATCCCACCAGGAG
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                                                          The invention relates to a G protein-coupled receptor (GPCR) IGS70

CC polypeptide including sequences that are 99-90.6% identical Also

CC included are the polymuclectide encoding IGS70 (including sequences 98-
99.6% identical to the polymuclectide or the DNA insert contained in
plasmid CBS 109818), a hybridisation probe derived from the

CC polymuclectide, a DNA or RNA expression system producing IGS70, a host

CC comprising the expression system, IGS70 receptor membrane preparation

derived from the cell, an antibody immunospecific for IGS70, IGS70 is

CC useful for diagnosing a disease or a susceptibility to disease in a

CC subject related to expression or activity of the IGS70 polypeptide in a

CC subject by determining the presence or absence of mutation in the

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CC subject by determining the presence or absence of mutation in the

CC subject by determining the presence or absence of mutation in the

CC antigonist The IGS70 protein, polynucleotide, antibody and identified

CC antigonists are useful for treating psychiataric and central nervous

CC failure, angina pectoris, myocardial infarction, kidney disease such as

CC failure, angina pectoris, myocardial infarction, kidney disease such as

CC failure, angina pectoris, myocardial disease, ulcers such as gastric ulcer,

CC inflammation, cancers, asthma, infection (such as bacterial, viral,

CHMO, diabetes, osteoporosis and allergies. The present sequence encodes

CC fundal protozoal) especially human immunodeficiency virus infection
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99.8%; Score 916.4; DB 6; Length 1051;
Best Local Similarity 99.9%; Pred. No. 1.1e-260;
Matches 917; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;
                          Claim 1; Page 6; 58pp; English.
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Antibacterial, virucide, fungicide, analgesic, antiparkinsonian, functional defects antiparkinsonian; generatory incurportective, noctropic; immunosuppressive, osteopathic, antibacterial; virucide, fungicide, analgesic, antiparkinsonian; GFCR; antipactatic, ophthalmologial; antitarginal; antithyroid; anticallergic; antipactatic; ophthalmologial; antitarginal; antithyroid; anticorrulsant; maintipactatic; antiarthritic; G-protein coupled receptor; subfamily I; maintipactor; immune; inflammatory disorder; plateled disorder; callular proliferative; differentiative disorder; hormonal disorder; cellular proliferative; differentiative disorder; hormonal disorder; neutological disorder; cardiovascular disorder; viral disorder; disorder; cardiovascular disorder; viral disorder; inver disorder; cardiovascular disorder; viral disorder; disorder; cardiopical disorder; cardior; disorder; disorder; cardiopical disorder; cardior; disorder; cardior; disorder; disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                840 AAGGITGCATITIATAAAGGAAATAITCITGAGIGIAACAGCAAITAGCIGCIAIGAITIG
                                                                                                                              TACCAGITCITTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
                                                                                                                                                                                                         TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
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/*tag= a
/product= "Human G-pr
93870"
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12380 CTICTCTITGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 12439
Human; ss; gene; G protein-coupled receptor; GPCR; IGS70; CNS; psychiatric disorder; central nervous system disorder; schizophrenia; Albahmer's disease; multiple sclerosis; anxiety; cardiovascular disease; heart failure; angina pectoris; myocardial infarction; kidney disease; renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS; inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer; asthma; infection; human immunodeficiency virus infection; HIV; diabetes; osteoporosis; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel G-protein coupled receptor IGS70 polypeptide useful for treating dysfunctions, disorders or disease related to lung, bone marrow, spinal cord immune system.
                                                                                                                                                                                                                                                                                                                                            12320 AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG
                                                                                                                                                                                                                                                12260 TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
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05-DEC-2000; 2000US-0251045P.
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P-PSDB; AAU99179.
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                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
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Best Local Similarity 100.0%; Pred. No. 4.5e-260;
Matches 918; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                        (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO
                                                                                                                                                                                                  Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1007; 28pp; English
                                                             18-JUN-2002; 2002EP-00013517.
                                                                                                    18-JUN-2001; 2001JP-00246789
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P-PSDB; ADC86555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses an isolated human polypeptide, and encoding nucleic acid, for a G protein-coupled receptor (GPCR), particularly the nucleic acid, for a G protein-coupled receptor (GPCR), particularly the communication between cells and their environment and are characterised by a serpentine structure that passes through the cell membrane seven times, hence the reason such receptors are sometimes called seven transmembrane receptors (7TM). The polynucleotides and polypeptides are useful for identifying an nothody that binds to an epitope of the polypeptide, for isolating an antibody that binds to an epitope of the polypeptide, for isolating an antibody that binds to be opypeptide or compound that binds the polypeptide or polynucleotide and/or modulates its biological activity, for screening a must polynucleotide and/or modulates its biological activity, for screening of thuman subject to diagnose a disorder, or a genetic predisposition to a compound that binds the polypeptide or identifying compounds useful for the treatment of a mental disorder, for identifying compounds useful as a modulator of binding between copperate in a mammal. The nucleic acid or negren inducing an immune response in a mammal. The nucleic acid or polypeptide is particularly useful, using gene therapy, for treating e.g. anxiety disorders, depression, bipolar disorder, schizophrenia, configuration of disease, dyskinesias, manic depression, stroke, Parkinson's disease, dyskinesias, manic depression, stroke, parkinson's disease or Alzheimer's disease. The nucleic acid and polypeptide may also be used for treating diabeters, inflammation or wounds. The sequences presented in ABS/0202-ABS/0248, ABS/0338 and ABS/0243 are the DNAs
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              Human; gene; ds; G protein-coupled receptor; GPCR; nGPCR; beGPCR; and grotein coupled receptor; communication; serventure structure; seven transmembrane receptor; 7TM; mental disorder; diagnosis; genetic predisposition; brain; immune response; gene therapy; anxiety disorder; depression; bipolar disorder; schizophrenia; Huntington's disease; dyskinesia; manic depression; stroke; Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids and polypeptides of the nG protein-coupled receptor, useful for treating or diagnosing a mental disorder or a disorder affecting the brain. e.g. anxiety disorders, schizophrenia, stroke or barkinson's disease.
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100.0%; Pred. No. 6e-261;
.ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                      Wood LS;
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                                                                                                                                                                                                                                                                                                                                                                   Vogeli G,
                                                                                                                                                                                                                                                                    14-FEB-2001; 2001WO-US004641.
                                                                                                                                                                                                                                                                                                    14-FEB-2001; 2001WO-US004641.
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P-PSDB; ABG93787.
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Best Local Similarity
Matches 918; Conserv
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                                                                                                                                  tranquiliser.
                                                                                                                                                                     Homo sapiens.
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CTCCTGGTGAAAATGAACACCCGGTCAGTGACCACCATGGCGGTCATTAACTTGGTGGTG
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                                                   ds; gene; human; \operatorname{GPCR}_i guanosine triphosphate-binding protein coupled receptor; gene therapy
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protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
I for diagnosing and treating e.g. schizophrenia.
neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rhumatoid arthittis; autoimmune disorder; respiratory ailment; neuroprotective; ds.
                                                                                                                                                                                                                                                                                                                                                                                     Parodi LA, Hiebsch RR, Lind P, Slightom J;
PS, Bannigan CM, Ruff V, Sejlitz T, Huff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 89-90; 261pp; English
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22 - ARR - 2000; 2000US - 0.18554P.
03 - MAR - 2000; 2000US - 0.186554P.
03 - MAR - 2000; 2000US - 0.18611P.
17 - MAR - 2000; 2000US - 0.198114P.
21 - MAR - 2000; 2000US - 0.19868P.
02 - ARR - 2000; 2000US - 0.198568P.
02 - MAY - 2000; 2000US - 0.203111P.
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Schellin KA, Kaytes
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P-PSDB; AAG80969.
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28-DEC-1999;
22-FEB-2000;
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                                                                                 Homo sapiens
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The present invention relates to novel G protein-coupled receptors (GDCRX; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 21-38, 40, 41, 53-60) and their coding sequences. The present sequence is the coding sequence for one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic form of predisposition, specifically schizophrenia. nGPCRx are useful for captures or identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a diagnostic tool for diseases or nGPCRx in a sample is useful as a diagnostic tool for diseases or nGPCRx in a sample is useful as a diagnostic tool for diseases or nGPCRx in a sample is useful as and hormonal disorders. Modulators of disease, proliferative disorders, renal failure, rheumatoid arbritis, including schizophrenia, AphDADD (attention deficit disorders such as Alzheimer's disease, pricible formation deficit disorders, and neuronal disorders such as Alzheimer's disease, prakinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arbritis, autolmmune disorders, cancers, concers, concers, concers.
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                                         CTCCTGGTGAAAATGAACACCCGGTCAGTGACCACCATGGCCGGTCATTAACTTGGTGGTG
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100.0%; Score 918; DB 4; Length 2525; 100.0%; Pred. No. 6e-261; ive 0; Mismatches 0; Indels 0

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DNA encoding human G protein-coupled receptor, nGPCR-16

Best Local Similarity 100. Matches 918; Conservative

642 360 702 420 762 480 822 540 882 9 942 9

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GICTICATCATTATGITGATGGIGCAGAAGCTACGCCACTCTTACTATCCCACCAGGAG 1002
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                                              CTCCTGGTGAAAATGAACCCCCGGTCAGTGACCACCATGGCCGCTCATAACTTGGTGGTG
                                                                                               GTCCACACACGCTTTTTCTGCTGACACTGCCATTTCGCTTGACCTCACCTCATCAACAAGAAGACT
                                                                                                                                     TGGATGTTTGGGCTGCCTTCTGCAAATTTGTGAGTGCCATGCTGCACATCTACATGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel polypeptides which have anti-HIV, antiatteriosclerotic, cytostatic, neuroprotective, antiparkinsonian, hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide, antibacterial, fungicide and protozoacide activity. The products of the invention are useful for treating a disease or condition associated with decreased expression or over expression of functional G-protein coupled receptors (GCREC), while antibodies generated against the polypeptide of with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer, stroke, Alahaimer's disease, Parkinson's disease, Crohn's disease, constipation, ALDS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy. AAF88580-AAF8851 encode the GCREC proteins represented by AAB71322-AAB71359, described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                     Tribouley CM, Nguyen DB, Thornton M, Yao MG, Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia AJA; Pel J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM; Malsh RT, Yes Na Richardson TW, Griffin JA; Yang J, Lee EA, Harland L;
                                                                  GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic; cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative; cerebroprotective; antiinflammatory; virucide; antibacterial; fundicide; protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS; Parkinson's disease; AIDS; gene therapy; gene; 88.
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100.0%; Score 918; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 4.5e-261;
Matches 918; Conservative 0; Mismatches 0; Indels 0
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                                              GCREC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54.
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23-FEB-2001; 2001US-027121SP.
08-MAR-2001; 2001US-0274551P.
23-MAR-2001; 2001US-0276507P.
02-APR-2001; 2001US-0280597P.
02-APR-2001; 2001US-0281507P.
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Kallick DA, Gandhi AR,
Ramkumar J, Pei J, Tar
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CTTCTCTTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT
                                                                                  TACCAGTICITTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
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ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGGGTGTCATTTCCATTCTTTTC 120

ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA 402

ATGCCTGGCCACATACCTCCAGGAATTCCTTGCGATCCTATAGTGACACCCCACTTA

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Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;
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23-FEB-2001; 2001US-0271215P.
08-MAR.-2001; 2001US-0274551P.
23-MAR.-2001; 2001US-0278507P.
02-APR.-2001; 2001US-0280597P.
06-APR-2001; 2001US-0281107P.
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AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG
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                                                                          1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA
                                                                                                                                                         61 ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGGGTGTCATTTCCATTTTTT
                 Pred. No. 4.3e-261;
; Mismatches 0;
100.08;
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                 Best Local Similarity 100.
Matches 918; Conservative
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                                                                                                                                                                                                                                                                     owner; human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic; cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative; cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide; protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AlDS; Parkinson's disease; Crohn's disease; constipation; infection; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel polypeptides which have anti-HIV, antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian, hepatotropic, laxative, cerebroprotective, antihfalmmacrory, virucide, antibacterial, fungicide and protozcacide activity. The products of the invention are useful for treating a disease or condition associated with decreased expression or over expression of functional G-protein coupled receptors (GCREC), while antibodies generated against the polypeptide of the invention are useful for diagnosing a condition or disease associated with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer, etroke, Alzheimer's disease, Parkinson's disease, constipation, ALDS, or bacterial, viral, fungal or protozcal infections. The compounds described in the invention can be used for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG; Kallick DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS, Hafalia AJA; Rankumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM; Graul RC, Khan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA; Warren BA, Yang J, Lee EA, Harland L;
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                 BP
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600 822 9

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standard; cDNA; 1460 AAF88585 **AAF**88585 RESULT 8
AAF88585
ID AAF8
XX
AC AAF8

Length 1340;

DB 6;

Score 918;

1002

1062

stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease, constipation, AIDS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy. AAR88580-AAF88627 encode the GCREC proteins represented by AAB71322-AAB71369, described in the disclosure of the invention

Sequence 1336 BP; 340 A; 289 C; 287 G; 420 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tribouley CM, Nguyen DB, Thornton M, Yao MG;
Gandhi AR, Walia NK, Arrizu C, Elliott VS, Hafalia AJA;
Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;
Atan FA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
Yang J, Lee EA, Harland L;
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or
                AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTGCTTTG
                                                                         CITCITTGCITTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT
                                                                                                   New human G-protein coupled receptors (GCREC), useful for diagnosing treating a disease or condition associated with decreased expression over expression of functional GCRECs e.g. cancer, Alzheimer's and parkinson's.
                                                                                                                                                                                                                                                                                                                                                                                                                CDNA INCYTE ID 90012430CD1 SEQ ID 52
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2001US-0271215P.
2001US-0274551P.
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2001US-0280597P.
2001US-0280597P.
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P-PSDB; AAB71325.
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Kallick DA,
Ramkumar J,
Graul RC, Kh
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                                                          ATCAGCCTCTACATCATAGTGCTTATTGGCGGGCTGGTGGTGTCATTTCCATCTTTTC
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Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-261;
Matches 918; Conservative 0; Mismatches 0;
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                                                                                                                                 CTTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT
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antinflammatory, antiasthmatic, antirheumatic or antiarthritic. The GAVE18 receptor and the DNA sequence encoding it may be a target for antisense therapy or gene therapy. The nucleic acid molecule, GAVE18 proteins and antibodies may be useful in screening assays, detection assays (for example chromosomal mapping, tissue typing or forensic biology), or predictive medicine (for example diagnostic assays, prognostic assays, montoring clinical trials and pharmacogenomics. The nucleic acid molecule, GAVE18, anti-GAVE18 anti-GAVE18 anti-bodies, agonist, inverse agonist and antagonist are also useful for preventing and treating a disease or disorder associated with abearant expression or activity of GAVE18, such as inflammation and immunological-related diseases or disorders for example asthma, chronic obstructive pulmonary disease or ineumatoid arthritis. The present sequence is the DNA sequence encoding the GAVE18 protein of the invention
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Best Local Similarity 100.0%; Pred. No. 3.7e-261;
Matches 918; Conservative 0; Mismatches 0; Indels
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The invention provides new G-protein coupled receptor (GPCR) polypeptides designated TGR2, TGR38, TGR18, TGR164, TGR343 and TGR358 and encoding polynucleotides. The polypeptides can be expressed by standard DNA recombination methodology. The polypeptides are useful for screening or identifying modulators of GPCR or signal transduction. The modulators of signal transduction are useful for treating or preventing TGR-associated disorders, e.g. asthma, multiple sclerosis or kidney disease. The polypeptides are useful as tragets for diagnosing or treating e.g. epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia, asymptomatic urinary abnormalities, hypertension, nephrolithiasis, cirrhosis, lesions, laundice, psoriasis, lupus erythematosus, or acute inflammatory dermatoses. The present sequence represents a human TGR343
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New G-protein coupled receptor polypeptides designated TGR2, TGR38, TGR118, TGR164, TGR343 and TGR358, useful as targets for screening drugs for treating or preventing e.g. asthma, multiple sclerosis, stroke or nephrolithiasis.
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Matches 918; Conservative 0; Mismatches 0;
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The present invention provides the protein and coding sequences of several human G-protein coupled receptors (GPCRs). These can be used in the identification of candidate compounds as receptor agonists or inverse agonists having applicability as therapeutic agents. The present sequence is a GPCR coding sequence of the invention
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Human, G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31; hRUP32; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
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20-FEB-2001; 2001US-0270266F.
20-FEB-2001; 2001US-0270286F.
06-APR-2001; 2001US-0282356F.
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The present invention provides the protein and coding sequences of a novel human testis-oxiginated G protein-coupled receptor protein TGR10. The sequences can be used in the development of drugs for the treatment of diseases of the central nervous system, inflammations, diseases of the circulatory system, cancer, metabolic diseases, immunological diseases, and diseases of the gastrointestinal system. The present sequence is the coding sequence of the invention
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This sequence encodes a human G-protein coupled receptor (GPCR), PFI-021. Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA libraries from peripheral blood monouclear cells. Two ESTS have been identified in libraries derived from breast mRNA. PFI-021 and the corresponding cDNA are used to treat a patient needing altered activation or expression of a GPCR, such as inflammation, allergy and respiratory, neurology, psychology, urogenital disease, reproductive and sexual dysfunction/disorders, cancer, tissue repair, dermatology, skin apgeneration disorders, photoageing, frailty, osteoprossis, metabolic disease, cardiovascular disease, gastro- intestinal disease, anti-infection, sensory organ disorders, sleep disorders and hair loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buch
                                                                                                                                                                                                                                          Gene; human; G-protein coupled receptor; GPCR; PFI-021; peripheral blood monouclear cell; PBMC; breast; inflammation; allergy; respiratory; neurology; psychology; urogenital disease; reproductive dysfunction; sexual dysfunction; cancer; tissue repair; dermatology; skin pigmentation; photoageing; frailty; osteoporosis; metabolic disease, cardiovascular disease; sleep disorder; hair loss; gastrointestinal disease; anti-infection; sensory organ disorder; ss.
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                                                                                                                 ABA00160 standard; cDNA; 918
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## ALIGNMENTS

Human testis originated G-protein coupled receptor TGR10 coding sequence. ВР. AAL44713 standard; DNA; 918 (first entry) 03-MAY-2002 AAL44713; RESULT 1 AAL44713

Human; testis-originated G-protein coupled receptor; TGR10; inflammatory; vycostatic; immunomodulaters; cardiant; neuroprotective; gene therapy; inflammation; nervous system disease; circulatory system disease; cancer; metabolic disease; immunological disease; gastrointestinal disease; gene;

Location/Qualifiers
1. .918
/\*tag= a
/product= "TGR10" Homo sapiens

15-JUN-2000; 2000JP-00184596 19-JUL-2000; 2000JP-00223887 14-JUN-2001; 2001WO-JP005061 WO200196567-A1 20-DEC-2001. 

Moriya T, Ito T, Shintani Y, Miyajima N; WPI; 2002-098071/13. P-PSDB; AAM48989.

(TAKE ) TAKEDA CHEM IND LTD

e.g. Human testis-originated G protein-coupled receptor protein TGR10 and encoded DNA, useful for gene diagnosis and developing drugs to treat diseases of central nervous system, inflammations and diseases of circulatory system.

Claim 5; Page 99; 110pp; Japanese

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New G-protein coupled receptor used in receptor assays as a target for diagnosis and treatment of receptor-mediated disorders, e.g. immune and inflammatory disorders, platelet disorders, skeletal or bone metabolism
                                                                                                               Claim 5; Page 101-103; 105pp; English
     28-FEB-2002; 2002WO-US006455.
                 01-MAR-2001; 2001US-0272677P
                               (MILL-) MILLENNIUM PHARM INC
                                                         WPI; 2002-732793/79
                                                                P-PSDB; AA022919
                                             Glucksmann MA;
                                                                                                  disorders
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The invention relates to an isolated polypeptide, which is a G-protein coupled receptor (GPCR) related to Subfamily I of G-protein coupled coupled receptor type proteins (GPCRs), designated the 93870 receptor. The polypeptides, nucleic acid molecules and antibodies of the invention are polypeptides, nucleic acid molecules and antibodies of the invention are monitoring clinical trials or pharmacogenetics), or in methods of treatment (e.g. therapeutic and prophylactic). They are useful in the plants of the 93870 polypeptides or nucleic acids, e.g. immune and inflammatory disorders, platelet disorders, skeletal or bone metabolism cinflammatory disorders, platelet disorders, skeletal or bone metabolism disorders, and fearname and/or differentiative disorders, normoral disorders, cardiovascular disorders, viral diseases, harmonial disorders, nucleic disorders, and pain and metabolic disorders. Conditions that can be created include cancer, diabetes mellitus, hypochyrodism, cancer, disease, mellitus, hypochyrodism, chromatodism, reproductive or fertility disorders, HIV, bacterial or viral meningitis, fungal meningoencephalitis, multiple sclerosis, conflammatory bowel disease, parkinson's disease, ataxia-telanglectasia, thurtington's disease, parkinson's disease, aschma, conjunctivitis, graft-versus-host disease, allergy, idiopathic thrombocytopenia, or osteoporosis. The transgenic animals are useful for studying the function and/or activity consense the anneal or desired sequence represents the 93870 pacterin and for identifying and/or evaluating modulatorse of a 93870 pacterin and for identifying and/or evaluating modulatorse of a 93870 pacterin and for identifying sequence represents the 93870 nucleotide sequence represents the 93870 nucleotides of the invention and or be useful for studying the protein of the invention of the invention Sequence 939 BP; 215 A; 212 C; 205 G; 307 T; 0 U; 0 Other;

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Query Match 94.1%; Score 864; DB 6; Length 939; Best Local Similarity 99.9%; Pred. No. 0; Matches 914; Conservative 0; Mismatches 1; Indels
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i TGTGTTTTGTGCCGT 939	925	g G
TGTGTTTTGTGCCGT 915	901	ò
S CTICTCTTTGTGTGTGTAAGCCATTGTTTTAAGCAAAAGATAATTGGCTTATGGAAT 924	865	qq
CTTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT 900	841	ò
s AAGGIIGCAITITTATAACGAAATCIICTTGAGIGTAACAGCAATTAGCTGCTATGATTIG 864	808	셤
AAGGTIGCAITITITATAACGAAAICTICTIGAGTGTAACAGCAATTAGCTCCTATGATTIG 840	781	ò
: TACCAGIICTITAGGAICTATTACTIGAATGITGIGACGCATICCAAIGCCTGTAGCAGC 804	745	ОÞ
TACCAGTICTITAGGALCTATTACTIGAATGITGIGACGCATTCCAATGCCTGTAACAGC 780	721	à
TTCTGGGCTCAGCTGAAAACCTATTTTTATAGGGGTCATCCTTGTTTGT	685	qq
TICTGGGCTCAGCTGAAAAACCTATTTTTATAGGGGTCATCCTTGTTTGT	661	ò
GTCTTCATCATTATGTTGATGGTGCAGAAGCTACGCCACTCTTTACTATCCCACCAGGAG 684	625	qq
GTCTTCATCATTATGTTGATGGTGCAGAAGCTACGCCACTCTTTACTATCCCACCAGGAG 660	601	ò
S ATCAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG 624	565	셤
ACAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTTCCTG 600	541	ò
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. ACGCTGGTGATTGTCATTGTGGTACCCCTGGTTGTCTCCCCGGTATGGAATCCATGAGGAA 504	445	q
ACCCTGGTGATTGTCATTGTGGTACCCCTGGTTGTCTCCCCGGTATGGAATCCATGAGGAA 480	421	δ
AAAGACAAAGTGGAATTCTACAGAAAACTGCATGCTGTGTGTG	385	qq
AAAGACAAAGIGGAATICIACAGAAAACIGCAIGCIGGGGGGGCGGCCAGIGCIGGGA120	361	δ
CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAGTGC 384	325	qa
CTCACGITCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC 360	301	ઠે

Search completed: April 25, 2004, 18:01:46 Job time : 454 secs

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The invention relates to an isolated polypeptide, which is a G-protein coupled receptor (GPCR) related to Subfamily I of G-protein coupled receptor type proteins (GPCRs), designated the 93870 receptor. The polypeptides, nucleic acid molecules and antibodies of the invention are useful in screening classes, predictive medicine (e.g. diagnostic assays, control of the 93870 polypeptides of in methods of treatment (e.g. therapeutic and prophylactic). They are useful in treatment (e.g. therapeutic and prophylactic). They are useful in treatment (e.g. therapeutic and prophylactic). They are useful in the 93870 polypeptides or nucleic acids, e.g. immune and inflammatory disorders, platelet disorders, skeletal or bone metabolism disorders, or bone marrow monounclear disorders, as well as cellular conditions and/or differentiative disorders, viral diseases, liver proliferative and pain and metabolic disorders, viral diseases, liver disorders, and pain and metabolic disorders, conditions that can be reproductive or fertility disorders, HIV, bacterial or viral meningitis, fungal meningoencephalitis, multiple sclerosis, contringents disease, parkinson's disease, asthma, conjunctivitis, graft-versus-host inflammatory bowel disease, asthma, conjunctivitis, graft-versus-host changesnic animals are useful for studying the function and/or activity condisease, allergy, idiopathic thromboytopenia, or osteoporosis. The transgenic animals are useful for studying the function and/or activity condisease, allergy, idiopathic thromboytopenia, or osteoporosis. The condisease, asthma, conjunctivity, graft-versus-host changenic animals are useful for studying the function and of or identifying and/or evaluating modulators of a 93870 protein and for identifying and/or evaluating modulators of condition and be used in continued therapy. This polynucleotide sequence represents the cDNA of the invantion
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Anti-HIV, cytostatic, antidiabetic, antiasthmatic; antiinflammatory;

Mantibacterial, virucide; funglicide; antiasthmatic; antipatatic; osteopathic;

KW antibacterial; virucide; funglicide; analgasic; antipatkinsonian; gPCR;

artibacterial; virucide; funglicide; analgasic; antiallergic;

KW antipsoriatic; ophthalmologial; antiinformal; antitallergic;

KW antipsoriatic; antiarthritic; G-protein coupled receptor; subfamily I;

KW antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;

KW antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;

KW antirheumatic; antiarthritic; G-protein coupled receptor; subfamily I;

KW play oreceptor; immune; inflammatory disorder;

KW meurological disorder; cardiovascular disorder;

Inver disorder; metabolic disorder; cancer; diabetes mellitus; bacterial;

Nothyroidism; hyperthyroidism; reproductive; ferrility disorder;

Nytochyroidism; hyperthyroidism; reproductive; ferrility

Nytochyroidism; hyperthyroidism; reproductive; ferrility

Nytochyroidism; hyperthyroidism; reproductive; ferrility;

Nytochyroidism; hyperthyroidism; reproductive; ferrility;

Nytochyroidism; hyperthyroidism; reproductive; dermatitis;

Nytochyroidism; hyperthyroidism; graft-versus-host disease;

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/product= "Human G-protein coupled receptor type protein
93870"
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541 ATCAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG
                                    711 ATCACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG
                                                                                                                                                                             939 nt coding DNA of a human G-protein coupled receptor type protein.
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cc derived from the cell, an antibody immunospecific for IGS70, IGS70 is useful for diagnosing a disease or a susceptibility to disease in a cc subject related to expression or activity of the IGS70 polypebtide in a cubject by determining the presence or absence of mutation in the concision from the subject. IGS70 is also useful identifying agonist cor antagonist. The IGS70 protein, polymucleotide, antibody and identified ant/agonists are useful for treating psychiatric and central nervous cor antagonists are useful for treating psychiatric and central nervous cor antiple sclerosis, anxiety, cardiovascular diseases such as heart cor antiple sclerosis, anxiety, cardiovascular diseases such as heart cor antiple sclerosis, anxiety, cardiovascular diseases such as heart cor and failure, againmentorined disease, ulcers such as gastric ulcer, inflammation, cancers, asthma, infection (such as bacterial, viral, fungal, proteozal) especially human immunodeficiency virus infection (HIV), diabetes, osteoporosis and allergies. The present sequence encodes the human GPCR IGS70
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Sequence 1051 BP; 244 A; 231 C; 230 G; 346 T; 0 U; 0 Other;

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120 179 239 240 1GGATGTTTGGGCTGCCCTTCTGCAAATTTGTGAGTGCCATGCTGGACATCCACATGTAC 300 360 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC 419 420 ACGCTGGTGATTGTCATTGTGGTACCCCTGGTTGTCTCCCGGTATGGAATCCATGAGGAA 480 540 600 9 719 Trenggereagergaaaacerarrrrraragggereareerrgrrgrreerreer 779 119 CICCIGGIGAAAAIGAACACCCGGICAGIGACCACCAIGGCGGICATIAACTIGGIGGIG 180 299 479 539 599 629 720 TACCAGITCTITAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC 780 recaretricederecerrerecaaarrrereaerecearecrecaerecaererae 359 9 GTCTTCATCATTATGTTGATGGTGCAGAGCTACGCCACTCTTACTATCCCACCAGGAG ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGTGGTGGTCTTTCCATTTCTTTTC CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC AAAGACAAAGTGGAATTCTACAGAAAACTGCATGTGGCTGCCAGTGCTGGCATGTGG Accerdendantercantercenacecendenterececeerarcaanceardaggaa ATCAACTATATGATAGTCATTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG ATCAACTATATGATAGTCATTTTTTGTCATAGCCGTTGCTGTGATTCTGTTGGTCTTCCAG GTCTTCATCATTATGTTGATGGTGCAGAAGCTACGCCACTTTTACTATCCCACCAGGAG 1 ATGCCTGGCCACAATACCTCCAGGAATTCCTCTTGCGATCCTATAGTGACACCCCACTTA TICTGGGCTCAGCTGAAAACCTATITITIATAGGGGTCATCCTTGTTTGTTTCCTTCCC ö 94.4%; Score 867; DB 6; Length 1051; 99.9%; Pred. No. 0; cive 0; Mismatches 1; Indels ( Best Local Similarity 99.9 Matches 917; Conservative 9 120 180 240 300 360 420 421 480 540 .009 61 121 181 241 361 481 541 099 720 301 601 661 721

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Mamostatic, neuroprotective, noctropic; immunosuppressive, osteopathic;

KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;

KW antibacterial; virucide; fungicide; analgesic; antiparkinsonian; GPCR;

KW antipsoriatic; ophthalmologial; antianginal; antichyroid; anticonvulsant;

KW antirheumatic; antiarthritic; G-protein coupled receptor; subfamily 1;

KW antirheumatic; immune; inflammatory disorder; platefat disorder;

KW skeletal; bone metabolism disorder; bone marrow mononuclear disorder;

KW cellular proliferative; differentiative disorder; hormonal disorder;

KW hypothyroidism; hyperthyroidism; reproductive; fertility disorder;

KW hypothyroidism; hyperthyroidism; reproductive; fertility disorder;

KW hypothyroidism; hyperthyroidism; reproductive; fertility disorder;

KW hypothyroidism; hyperthyroidism; reproductive; dertility disorder;

KW hypothyroidism; hyperthyroidism; supribe sclerosis;

KW huntington's disease; heart failure; angina pectoris; dermatitis;

KW myocardial infarction; rheumatord arthritis; psoriaatis;

KW myocardial infarction; rheumatord arthritis; psoriaatis;

KW myocardial infarction; rheumatord arthritis; psoriaatis;

KW myocardial infarction; rheumatord asthma; graff-vergus-host disease;

KW transgenic animal; human; gene; ss.
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/*tag= a
/product= "Human G-protein coupled receptor type protein
93870"
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TACCAGTICTITAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
                                                                                                                                                                                                                                        CTTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel G-protein coupled receptor IGS70 polypeptide useful for treating dysfunctions, disorders or disease related to lung, bone marrow, spinal cord immune system.
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                                  TACCAGTICITTAGGAICTATTACTIGAATGTIGTGACGCATTCCAATGCCTGTAACAGC
                                                                                                                                                              AAGGITGCATITIATAACGAAATCITCTIGAGIGTAACAGCAATTAGCIGCTAIGATTIG
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/product= "GPCR IGS70"
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2000US-0251045P.
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                                                                                      Novel G-protein coupled receptor polypeptides referred as GCREC peptides, useful for treating multiple sclerosis, cholecystitis heart failure, angina pectoris, rheumatoid arthritis, obesity, osteoporosis.
                                                                                                                                                                                                  The invention relates to human G-protein coupled receptor (GCREC 1-16) polypeptides and polynucleotides. Sequences of the invention are useful for the diagnosis, treatment and prevention of cell proliferative (e.g. cancer, cirrhosis), neurological (e.g. multiple sclerosis, Huntington's disease, Alzheimer's disease), cardiovascular (e.g. angina pectoris, heart failure), gastrointestinal (e.g. anorexia, cholecystitis), autoimmune/inflammatory (rheumatoid arthritis, Hashimoto's thyroiditis) and metabolic disorders (e.g. obesity, osteoporosis), viral infections, atherosclerosis and hepatitis. GCREC proteins are useful for identifying compounds that modulate, mimic and block olfactory and taste sensations. They are also useful for identifying GCREC modulators. GCREC DNAs are useful in gene therapy. The present sequence is human GCREC-6 CDNA
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Policky JL;
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Pred. No. 0;
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DAM,
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Best Local Similarity 100.
Matches 887; Conservative
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                                                          P-PSDB; AAE23414.
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Nguyen DB,
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                                                              601 GICTICATCATIAIGIIGAIGGIGCAGAAGCIACGCCACICTITACIAICCCACCAGGAG
                                                                                       GICTICATCATTATGITGATGGTGCAGAAGCTACGCCACTCTTTACTATCCCACCAGGAG
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Tribouley CM, Thornton M, Kallick DA, Yao MG;
Burford N, Khan FA, Yue H, Lu Y, Arvizu C, 1
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381. 1400
/*teg= a /product= "Human GCREC-6 protein"
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13-CTT-2000; 2000US-0249589P.
20-CCT-2000; 2000US-0243223P.
03-NOV-2000; 2000US-0245855P.
03-NOV-2000; 2000US-024580P.
15-NOV-2000; 2000US-024580P.
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Ramkumar J,
Elliott VS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11840 CTCACGTTCCTATTCTATGTGGTGATCCTGGTCACCAGATACCTCATCTTCTTCAAGTGC 11899
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                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
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                                                                                                                                                                                                                                                                                                          New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
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ive 0; Mismatches
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                                                                  18-JUN-2002; 2002EP-00013517.
                                                                                                           18-JUN-2001; 2001JP-00246789
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Matches 918; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses an isolated human polypeptide, and encoding nucleic acid, for a G protein-coupled receptor (GPCR), particularly the nucleic acid, for a G protein-coupled receptor (GPCR), particularly the communication between cells and their environment and are characterised communication between cells and their environment and are characterised by a serpentine structure that passes through the cell membrane seven times, hance the reason such receptors are sometimes called seven cransmembrane receptors (7TM). The polynucleotides and polypeptides are useful for identifying an nGPCR allelic variant that correlates with a content disorder, for isolating an antibody that binds to an epitope of the polypeptide for identifying a compound that binds to an epitope of the polypeptide and/or modulates its biological activity, for screening a copyrucleotide and/or modulates its biological activity, for screening a disorder to disprace to disprace in a genetic predisposition to the disorder. Cor identifying compounds useful for the treatment of a mental disorder and for identifying compounds useful for the treatment of a mental disorder. Go inducing an immune response in a mammal. The nucleic acid or polypeptide is particularly useful, using gene therapy, for treating e.g. anxiety disorders, depression, bipolar disorder, schizophrenia, chuntington's disease, dyskinesias, manic depression, stroke, Parkinson's disease or Alzheimer's disease, The nucleic acid and polypeptide may also be used for treating diabetes, inflammation or wounds. The sequences presented in ABS70222-ABS70248, ABS70318 and ABS70243 are the DNAs
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         Human; gene; ds; G protein-coupled receptor; GPCR; nGPCR; beGPCR; nG protein coupled receptor; communication; serpentine structure; seven transmembrane receptor; 7TM; mental disorder; diagnosis; genetic predisposition; brain; immune response; gene therapy; anxiety disorder; depression; bipolar disorder; schizophrenia; Huntington's disease; dyskineaia; manic depression; stroke; parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCAGCCTCTACTTCATAGTGCTTATTGGCGGGCTGGTGGTGTCATTTCCATTTCTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids and polypeptides of the nG protein-coupled receptor, inl for treating or diagnosing a mental disorder or a disorder or eting the brain, e.g. anxiety disorders, schizophrenia, stroke or
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                                                                                                                                                                                                                                                                                                                                                    (PHAA ) PHARMACIA & UPJOHN CO
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guanosine triphosphate-binding protein coupled receptor; gene therapy.
TGGATGTTTGGGCTGCCTTCTGCAAATTTGTGAGTGCCATGCTGCACATGTAC
                                                                                              TGGATGTTTGGGCTGCCCTTCTGCAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC
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27 AIGCCIGGCCACAAIACCTCCAGGAAITCCTCTIGGGATCCTAIAGTGACACCCCACTIA

147 CICCIGGIGAAAAIGAACACCCGGICAGIGACCACCACCATGGCGGICAITAACIIGGIGGIG

CTCCTGGTGAAAATGAACACCCGGTCAGTGACCACCATGGCGGTCATTAACTTGGTGGTG

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GICCACACACGCTITITCIGCTGACAGICCCATITCGCTTGACCTACCTCAAGAAGACT

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267 TGGATGTTTGGGCTGCCCTTCTGCAATTTGTGAGTGCCATGCTGCACATACCACATGTAC

TGGATGTTTGGGCTGCCCTTCTGCAAATTTGTGAGTGCCATGCTGCACATCCACATGTAC

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The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is the coding sequence of sequence for one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal cransduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. NGPCRx are useful for predisposition, specifically schizophrenia. NGPCRx are useful for nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention defici-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alabiment's disease, prollide inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory aliments such as asthma, and inflammatory diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia.
neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff I
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17-NOV-1999; 99US-0166071P.
19-NOV-1999; 99US-0166071P.
28-DEC-1999; 99US-0173396P.
28-FEB-2000; 2000US-0184129P.
28-FEB-2000; 2000US-0184129P.
28-FEB-2000; 2000US-0185421P.
28-FEB-2000; 2000US-0186531P.
09-MAR-2000; 2000US-0186114P.
17-MAR-2000; 2000US-019810P.
21-MAR-2000; 2000US-019810P.
21-MAR-2000; 2000US-019810P.
20-MAY-2000; 2000US-019868P.
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25-MAY-2000; 2000US-019868P.
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This invention describes novel polypeptides which have anti-HIV, antiarteriosclerotic, cytostatic, neuroprotective, antiantamentory, virucide, hepatotropic, laxative, cerebroprotective, antiantlammatory, virucide, antibacterial, fungicide and protozoacide activity. The products of the invention are useful for treating a disease or condition associated with decreased expression or over expression of functional d-protein coupled receptors (GCREC), while antibodies generated against the polypeptide veceptors (GCREC), while antibodies generated against the polypeptide with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease, constipation, AIDS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy. AAPR88580-AAF88627 encode the GCREC proteins represented by AAB71322-AAB71359, described in the disclosure of the invention
                                                                                           GCREC; Human, G-protein coupled receptor; anti-HIV; antiarteriosclerotic; cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative; cerberoprotective; antihiflammatory; virucide; antibacterial; fungicide; protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS; Parkinson's disease; Crohn's disease; constipation; infection;
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Kallick DA, Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia AJA;
Rankumar J, Pei J, Tang YT, Yue H, Reddy R, Butford N, Lu DAM;
Graul RC, Khan PA, Walsh RT, Ison CH, Richardson TW, Griffin JA;
Warren BA, Yang J, Lee EA, Harland L;
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                                                       Human GCREC-6 cDNA INCYTE ID 90012670CD1 SEQ ID 54
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23-FEB-2001; 2001US-0271215P.
08-WAR-2001; 2001US-027451P.
23-WAR-2001; 2001US-0286507P.
30-WAR-2001; 2001US-0286597P.
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This invention describes novel polypeptides which have anti-HIV, hepatotrotropic, cytostatic, neuroprotective, antiparkinsonian, hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide, antibacterial, fungicide and protozoacide activity. The products of the invention are useful for treating a disease or condition associated with decreased expression or over expression of functional G-protein coupled receptors (GCREC), while antibodies generated against the polypeptide of with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer, strok, Alzheimer's disease, arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, barkinson's disease, Crohn's disease, constipation, AIDS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy. AAPR98580-AAR98527 encode the GCREC proteins represented by AAB71322-AAB71369, described in the disclosure of the invention
                                                                                                                                                                                 GCREC; Human, G-protein coupled receptor; anti-HIV; antiarteriosclerotic; cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative; cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide; protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS; Parkinson's disease; Crohn's disease; constipation; infection; gene therapy; gene; ss
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23-FEB-2001; 2001US-027121SP.
08-MAR-2001; 2001US-027451P.
23-MAR-2001; 2001US-0278507P.
02-APR-2001; 2001US-0280597P.
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Sequence 1340 BP; 321 A; 310 C; 291 G; 418 T; 0 U; 0 Other;

100.0%; Score 918; DB 6; Length 1340,

AAF88585 RESULT 8
AAF88585
ID AAF8
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AC AAF8 stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease, constipation, AIDS, or bacterial, viral, fungal or protozoal infections. The compounds described in the invention can be used for gene therapy. AAR88580-AAF88627 encode the GCREC proteins represented by AAB71322-AAB71369, described in the disclosure of the invention

Sequence 1336 BP; 340 A; 289 C; 287 G; 420 T; 0 U; 0 Other;

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CTTCTCTTTGTCTTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT
                                             CTICICITIGECTITICGGGGAAGCCATIGGITIAAGCAAAAGAIAATIGGCITAIGGAAT
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Gandhi AR, Walia NK, Arvizu C, Elliott VS, Hafalia A,
Pei J, Tang YI, Yue H, Reddy R, Butford N, Lu DAM,
Khan FA, Waleh RT, Ison CH, Richardson TW, Griffin JA;
Yang J, Lee EA, Harland L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human G-protein coupled receptors (GCREC), useful for diagnosing treating a disease or condition associated with decreased expression over expression of functional GCRECs e.g. cancer, Alzheimer's and Parkinson's.
                                                                                                                                                                                                                               Human GCREC-4 cDNA INCYTE ID 90012430CD1 SEQ ID 52.
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23-FEB-2001; 2001US-0271215P.
23-MAR.2001; 2001US-0274551P.
23-MAR.2001; 2001US-0278507P.
02-APR.2001; 2001US-0280597P.
06-APR-2001; 2001US-0281107P.
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Query Match 100.0%; Score 918; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 918; Conservative 0; Mismatches
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This invention describes novel polypeptides which have anti-HIV, antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian, hepatotropic, laxative, cerebroprotective, antiinflammatory, vinucide, antibacterial, fungicide and protozoacide activity. The products of the invention are useful for treating a disease or condition associated with decreased expression or over expression of functional G-protein coupled receptors (GCREC), while antibodies generated against the polypeptide of the invention are useful for diagnosing a condition or disease associated with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,

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                                                                                                                                                                                                                                                                                                                                                                                                               Human G-protein coupled receptor; GAVE18; signal transduction; inflammation; physiological immunological response; antiinflammatory; antiasthmatic; antishemmatic; antishemmatic; antishemmatic; antishems therapy; chromosomal mapping; tisue typing; forensic biology; predictive medicine; asthma; chronic obstructive pulmonary disease; COPD; rheumatoid arthritis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New GAVE18 polypeptide and nucleic acid molecule encoding the polypeptide, useful for preventing and treating a disease or disorder associated with aberrant expression or activity of GAVE18, e.g. asthma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel G-protein coupled receptor (GAVE18) that is involved in signal transduction in respect to inflammation and the physiological immunological response. Molecules which may modulate the signalling activity or signal transduction of the receptor may be
<u> AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG</u>
                                                    TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
                                                                     TACCAGTTCTTTAGGATCTATTACTTGAATGTTGTGACGCATTCCAATGCCTGTAACAGC
                                                                                                        AAGGTTGCATTTTATAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG
                                                                                                                                                             CTTCTCTTTGTCTTTGGGGGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAAT
                                                                                                                                                                                                                                                                                                                                                                                       Human G-protein coupled receptor GAVE18 DNA sequence.
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/*tag= a
/product= "GAVE18 protein"
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22-MAR-2002; 2002GB-00006891.
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P-PSDB; AAO27265.
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antiinflammatory, antiasthmatic, antirheumatic or antiarthritic. The GAVEI8 receptor and the DNA sequence encoding it may be a target for antisense therapy or gene therapy. The nucleic acid molecule, GAVEI8 proteins and antibodises may be useful in screening assays, detection assays (for example chromosomal mapping, tissue typing or forensic bloogy), or predictive medicine (for example diagnostic assays, monitoring clinical trials and pharmacogenomics. The prognostic assays, monitoring clinical trials and pharmacogenomics. The nucleic acid molecule, GAVEI8, anti-GAVEI8 antibodies, agonist, inverse agonist and antagonist are also useful for preventing and treating a GAVEI8, such as inflammation and immunological-related diseases or clisorders, for example asthma, chronic obstructive pulmonary disease or the GAVEI8 protein of the invention
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The invention provides new G-protein coupled receptor (GPCR) polypeptides designated TGR2, TGR38, TGR18, TGR164, TGR343 and TGR388 and encoding polynucleotides. The polypeptides can be expressed by standard DNA recombination methodology. The polypeptides are useful for screening or identifying modulators of GPCR or signal transduction. The modulators of signal transduction are useful for treating or preventing TGR-associated disorders, e.g. asthma, multiple sclerosis or kidney disease. The polypeptides are useful as targets for diagnosing or treating e.g. epilepsy, stroke, neurodegeneration, hypogonadism, hyperprolactinemia, asymptomatic utinary abnormalities, hypertension, nephrolithiasis, cirkhosis, lesions, laundice, psoriaais, lupus erythematosus, or acute inflammantoses. The present sequence represents a human TGR343
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New G-protein coupled receptor polypeptides designated TGR2, TGR38, TGR18, TGR164, TGR343 and TGR358, useful as targets for screening drugs for treating or preventing e.g. asthma, multiple sclerosis, stroke or nephrolithiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCTGGTGAAAATGAACACCCGGTCAGTGACCACCATGGCGGTCATTAACTTGGTG
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                                                                                                                                                                                                                                                                                                  Claim 7; Page 61; 74pp;
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Best Local Similarity
Matches 918; Conserve
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The present invention provides the protein and coding sequences of several human G-protein coupled receptors (GPCRs). These can be used in the identification of candidate compounds as receptor agonists or inverse agonists having applicability as therapeutic agents. The present sequence is a GPCR coding sequence of the invention
Human, G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37; gene; ss.
                                                                                                                                                                                                                                                                                                                                                         Novel endogenous and non-endogenous versions of G protein-coupled receptor useful for identification of candidate compounds as receptor agonists or antagonists for use as therapeutic agents.
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12-DEC-2001; 2000US-025556FP.
20-FEB-2001; 2001US-027026FP.
20-FEB-2001; 2001US-0282032P.
06-APR-2001; 2001US-0282356P.
06-APR-2001; 2001US-0282356P.
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The present invention provides the protein and coding sequences of a novel human testis-originated G protein-coupled receptor protein TGR10. The sequences can be used in the development of drugs for the treatment of diseases of the central nervous system, inflammations, diseases of the circulatory system, cancer, metabolic diseases, immunological diseases, and diseases of the gastrointestinal system. The present sequence is the coding sequence of the invention
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This sequence encodes a human G-protein coupled receptor (GPCR), FFI-021. Expressed sequence tags of the PFI-021 sequence are mainly found in cDNA ilbraries from peripheral blood monouclear cells. Two ESTs have been identified in libraries derived from breast mRNA. PFI-021 and the corresponding cDNA are used to treat a patient needing altered activation rexpectation and a GPCR, such as inflammation, allergy and respiratory, neurology, psychology, urogenital disease, reproductive and sexual dysfunction/disorders, cancer, tissue repair, dermatology, skin pigmentation disorders, photoagaing, frailty, osteoporosis, metabolic disease, cardiovascular disease, gastro- intestinal disease, anti-infection, sensory organ disorders, sleep disorders and hair loss
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peripheral blood monouclear cell; PBNC; breast; inflammation, allergy;
respiratory; neurology; psychology urogenital disease;
reproductive dysfunction; sexual dysfunction; cancer; tissue repair;
dermatology; skin pigmentation; photoageing; frailty; osteoporoeis;
metabolic disease; cardiovascular disease; sleep disorder; hair loss;
gastrointestinal disease; anti-infection; sensory organ disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w human G-protein coupled receptor involved in signal transduction,
eful to treat disorders associated with its expression or activity
inflammation, allergy and cancer.
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/product= "PFI-021"
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P-PSDB; AAG79446.
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PCR prime TagMan pr

Human G p Human nGP Oligonucl PCR prime

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Aah51055
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Abs70288
Abs70317
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Abs70318
Abs70319

PCR prime nGPCR-x r Human TGR Human G p Human G p

PCR prime nGPCR-x r Oligonucl Human nGP

Title: Perfect

Run on:

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Human; testis-originated G-protein coupled receptor; TGR10; inflammatory, cytostatic; immunomodulator; cardiant; neuroprotective; gene therapy; inflammation; nervous system disease; circulatory system disease; cancer; metabolic disease; immunological disease; gastrointestinal disease; gene;
                                                                                                                                                                                                                                                                                                                       Human testis originated G-protein coupled receptor TGR10 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human testis-originated G protein-coupled receptor protein TGR10 and encoded DNA, useful for gene diagnosis and developing drugs to treat diseases of central nervous system, inflammations and diseases of circulatory system.
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                           AAH51055
AAH51084
AAH51084
ABA570288
ABS70218
AAB570731
AAH51085
AAH51086
ABS70318
ABS70318
ABS70319
AAL44718
ABT04906
AAL57075
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/product= "TGR10"
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19-JUL-2000; 2000JP-00223887.
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 WPI; 2002-098071/13.
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                  3373863 seqs, 2124099041 residues
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AAH51009
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ADC86554
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Result No.

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Claim 5; Page 99; 110pp; Japanese.

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RESULT 14
US-09-489-039A-1185/c
US-09-489-039A-1185/c
Sequence 1185, Application US/09489039A
Factor No. 6610836
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMONOLIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREMONOLIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF ILING DATE: 2709-22004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-27
FRICK PAPLICATION NUMBER: US 60/117,747
FRICK FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1185
LENGTH: 978
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Sequence 461, Application US/0983381

Patent No. 6672186

GENERAL INFORMATION:

APPLICANT: RObison, Keith E.

TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs

FILE REPREBERGE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT APPLICATION NUMBER: 09/516,448

PRIOR PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SEQ ID NO 461

SEQ ID NO 461

EINGTH: 1057
                                              Gaps
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1.9%; Score 17; DB 4; Length 1057;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels
DB 4; Length 801; 73;
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                                              0; Indels
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1.9%; Score 17; DB 4;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches
Query Match 1.9%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 73; Matches 17; Conservative 0; Mismatches
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Job time : 95 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 ACCACCATGGCGGTCAT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 ACCACCATGGCGGTCAT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 615 GTTGATGGTGCAGAAGC 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           704 GITGATGGTGCAGAGC 720
                                                                                                                   18 TGTTTTAAATTTCACAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-833-381-461
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US-09-540-236-1026
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                                                                                                                                        Sequence 3, Application US/09734673

Sequence 3, Application US/09734673

Sequence 3, Application US/09734673

Sequence 3, Application US/09734673

GENERAL INFORMATION:
APPLICANT: GUBGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFREENCE: CLOOL020

CURRENT APPLICATION NUMBER: US/09/734,673

CURRENT PILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 6

SOTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LEMOTH: 38564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-313-294A-940

Sequence 940, Application US/09313294A

Sequence 940, Application US/09313294A

Sequence 940, Application US/09313294A

Sequence 940, Application

Sequence 940, Application

Sequence 940, Application

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lo, Laura Y.

APPLICANT: Lo, Laura Y.

APPLICANT: Lo, Laura Y.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

FILE REFERENCE: PL-0017 US

CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program

SEQ ID NO 940

LENGTH: 258
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100.0%; Pred. No. 24;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.9%; Score 17; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700550095H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34622 GITCCIATICIATGIGGT 34605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature;
CCATION: (1)...(38564)
COTHER INFORMATION: n = A,T,C or G
US-09-734-673-3
3981 TATTGGCGGGCTGGTGGG 3998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 18; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-313-294A-940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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RESULT 11 US-09-833-381-1029/c ; Sequence 1029, Application US/09833381 ; Patent No. 6672186

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Sequence 1020, Application US/09540236

Ratent No. 6673910

GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NOS: 3840
LENGTH: 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1026, Application US/09540236

Sequence 1026, Application US/09540236

Parent No. 6673910

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERSUE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

LENGTH: 648
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APPLICANT: Robison, Keith E.
APPLICANT: Robison, No. 6672186el Nucleic Acid and Protein Homologs.
TITLE OF INVENTION: NO. 6672186el Nucleic Acid and Protein Homologs.
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FeatSEQ for Windows Version 3.0
SEQ ID NO 1029
LENGTH: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 17; DB 4; Length 472;
100.0%; Pred. No. 72;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 4;
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                              ; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(472)

; OTHER INFORMATION: n = A,T,C or G

US-09-833-381-1029
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Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 TGAGTGCCATGCTGCAC 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; ORGANISM: M.catarrhalis
US-09-540-236-1026
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; ORGANISM: M.catarrhalis
US-09-540-236-1020
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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US-09-540-236-1020/c
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Sequence 9867, Application US/09252991A
Sequence 9867, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT:
MACJ OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
PRIOR PAPLICATION NUMBER:
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-05-259-991A-10198/C
US-05-252-991A-10198, Application US/09252991A
Sequence 10198, Application US/09252991A
Fatent No. 6551795
Fatent No. 6551795
FATENCANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PLILOR DATE: 1999-02-18
PRIOR PLILOR DATE: 1999-02-18
PRIOR PLILOR DATE: 1998-07-27
NUMBER OP SEQ ID NOS: 33142
SEQ ID NO 10198
LENGTH: 1311
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2.0%; Score 18; DB 4; Length 4248;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels
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2.0%; Score 18; DB 4; Length 1311;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                            Query Match
2.0%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches
               ; SEQ ID NO 3416
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10198
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9867
                                                                                                                                                                                                                                                                                                                                                                             611 TTATGTTGATGGTGCAGA 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 rhárdríchráchácháh 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 rarrescesecrecreses 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 TATTGGCGGGCTGGTGGG 101
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US-09-252-991A-9867
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Patent No. 6562958

APPLICANT: Gary L. Breton et al.

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUVANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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100.0%; Pred. No. 22;
ive 0; Mismatches 0; Indels
ALTURACATION NUMBER: 07/635,475
FILING DATE: 28-Dec-1990
APPLICATION NUMBER: 07/377,238
FILING DATE: 06-011-1984
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: TRV 2 005
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMY: (216) 241-1666
TELER: (216) 241-1666
TELER: (216) 280162
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 base pairs
TYPE: Nucleic acid
STRANDEDDESS: Single
TOPPLOGY: Linear
MOLECULE TYPE: Nucleotide-genomic DNA
HYPOTHETICAL: Irrelevant
ANTI-SENSE: Irrelevant
FRAGMENT TYPE: Endonuclease restriction
PRAGMENT TYPE: Endonuclease restriction
PRAGMENT TYPE: Endonuclease restriction
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAPLOTYPE: Irrelevant
TISSUE TYPE: Lung
CELL TYPE: Lung
CELL LINE: Irrelevant
ORGANBILE: Irrelevant
IMMEDIATE SOURCE:
LIBRARY: Human genomic in lambda
CLONE: F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COL4AS collagen gene
Exon 16 region from 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: Irrelevant
INDIVIDUAL ISOLATE: Irrelevant
DEVELOPMENTAL STAGE: Irrelevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:

| NAME/KEY: COL4A5 collage
| LOCATION: Exon 16 region
| LOCATION: end of gene
| LOCATION: end of gene
| LOCATION: end of gene
| COTHER INFORMATION: The
| COTHER INFORMATION: nucl
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CHROMOSOME/SEGMENT: X
MAP POSITION: q22
UNITS: Irrelevant
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COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: ZO KO
COMPUTER: IBM PS/2, W
OPERATING SYSTEM: DOS
                229 ATCAAGAAGAC
                                                    3923 ATCAAGAAGA
                                                                                                                             JS-09-252-991A-10058/c
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US-08-692-989-16
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APPLICANT: MINAZZONO, Kohei

APPLICANT: MINAZZONO, Hidenori

TITLE OF INVENTION: APOPTOSIS-INDUCING PROTEIN AND GENE ENCODING THE SAME

TITLE OF INVENTION: 19941/0117

CURRENT FAPLICATION NUMBER: US/09/171,410

CURRENT FILING DATE: 1998-10-19

EARLIER FILING DATE: 1996-010-19

EARLIER FILING DATE: 1996-08-23

EARLIER FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver: 2.0
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APPLICANT: Breet P. Monia
APPLICANT: Breet P. Monia
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: Lac M. Cowarde
TITLE OF INVENTION: ANTIENSE MODULATION OF MEKKS EXPRESSION
FILE REFERENT APPLICATION NUMBER: US/09/359,757
CURRENT PILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4533;
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  0; Indels
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7.2;
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    0; Mismatches
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; Sequence 1, Application US/09359757
; Patent No. 6080546
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                                                                            158 Arcaagagactrogardr 176
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LOCATION: 4687
CTHER INFORMATION: unknown
US-09-359-757-1
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LOCATION: (361)..(4485)
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; LOCATION: (268)..(4392)
US-09-171-410-2
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 19; Conserva
                                          229 ATCAAGAAGAC
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LENGTH: 5236
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LENGTH: 4533
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196.136
CURRENT APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10058
LENGTH: 258
TAPPE: TA
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| Patent No. 657649
| Patent No. 6576410|
| APPLICANT: Tryggvason, Karl APPLICANT: Tryggvason, Karl APPLICANT: Tryggvason, Karl APPLICANT: APPLICANT: Bou. Jing Sirka L. APPLICANT: APPLICANT: Method for Determining the TITLE OF INVENTION: Nucleotide Sequence of the Gene TITLE OF INVENTION: Nucleotide Sequence of the Gene TITLE OF INVENTION: Type IV Collagen
| TITLE OF INVENTION: Type IV Collagen NUMBER OF SEQUENCES: 23
| CORRESPONDENCE ADDRESS: ADDRESSE: Minnich & McKee STREET: 1100 Superior Avenue STREET: Suite 700
| CITY: Cleveland STATE: Ohio COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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2.0%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/346,336
FILING DATE: 29-NOV-1994
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APPLICATION NUMBER: US/08/692,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10058
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SEQUENCE CHARACTERISTICS:
    LENGTH: 263 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    IMMEDIATE SOURCE:
    LIBRARY: BRAINOT12
    CLONE: 1413041
US-09-016-434-168
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Best Local Similarity
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Sequence 2, Appli
Sequence 1, Appli
Sequence 10058, A
Sequence 3416, Appl
Sequence 3416, Appl
Sequence 9867, Ap
Sequence 940, Appl
Sequence 1029, Appli
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Sequence 310, App
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Sequence 1, Appli
                                                                                                                                                          April 25, 2004, 17:46:14 ; Search time 91 Seconds (without alignments) 5598.296 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents NA:*

1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-359-757-1
US-09-359-757-1
US-09-252-918-10058
US-09-252-918-10198
US-09-252-918-10198
US-09-313-254A-940
US-09-313-254A-940
US-09-313-254A-940
US-09-313-254A-940
US-09-313-254A-940
US-09-313-381-1029
US-09-833-381-461
US-09-833-381-461
US-09-833-381-461
US-09-833-381-461
US-09-833-381-461
US-09-976-594-310
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                                                                                                           OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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1.9 5280 4 US-08-956-1718-544 Sequence 5 11.9 269223 4 US-09-596-002-41 Sequence 4 11.9 269223 4 US-09-596-002-41 Sequence 4 11.9 269223 4 US-09-596-002-41 Sequence 4 11.9 786421 4 US-09-751-389-1 Sequence 2 11.9 1664976 4 US-09-751-389-1 Sequence 2 11.9 1830121 4 US-09-557-884-1 Sequence 2 11.7 208 4 US-09-322-32491 Sequence 2 11.7 208 4 US-09-313-294A-4045 Sequence 4 US-09-313-294A-4045 Sequence 5 11.7 503 4 US-09-51-126-133 Sequence 1 11.7 503 4 US-09-61-126-133 Sequence 1 11.7 513 1 US-08-462-894-15 Sequence 1 11.7 513 1 US-08-462-894-16 Sequence 1 11.7 513 1 US-08-862-894-16 Sequence 1 11.7 513 1 US-08-862-894-18 Sequence 1 11.7	ALIGNMENTS	SULT 1  Sequence 168, Application US/09016434  Sequence 168, Application US/09016434  Sequence 168, December 100  Sequence 168, Application US/09016434  Patent No. 6500938  APPLICANT: Janice Au-Young  APPLICANT: Jeffrey J. Seilhamer  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  TITLE OF INVENTION: PATHWAY GENE EXPRESSION  NUMBER OF SEQUENCES: 1490  CORRESPONDENCE ADDRESS: 1490  CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ADDRESSE: NOTTE FRARMACEUTICALS, INC.  STREET: 3174 PORTER DRIVE  CITY: PALO ALTO  STATE: CALIFORNIA  COUNTRY: USA  ZIP: 94304  COMPUTER READABLE FORM:  MEDIUM TYPE: RIOPPY disk  COMPUTER: IBM PC COMPATIBLE  COMPUTER: TEM PC COMPATIBLE  OPERATION SYSTEM: PC-DOS/NS-DOS  SOFTWARE: WORD Perfect 6.1 for Windows/MS-DOS 6.2  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/09/016,434  CLASSIFICATION  RESIFICATION  ATTORNEY/AGENT INFORMATION:  NAME: Zeller, Karen J.  RESIFICATION NUMBER: 37,071  RESIFICATION NUMBER: 37,071  RESIFICANTION NUMBER: 37,071
28 229 33 33 33 33 33 33 33 33 33 33 33 33 33		RESULT 1  108-09-016-434-168 108-09-016-434-168 108-09-016-434-168 108-08-08-08-08-08-08-08-08-08-08-08-08-0

Length 263;

DB 4; 6.8;

2.1%; Score 19; 100.0%; Pred. No.

Similarity: 46.57¢ Missatches: 128  Jacobs Holdis: 20  13.63¢ Missatches: 128  Indels: 27.08¢
Percent Simil Best Local Simil Best Local Simil Best Local Signing of the control

Search completed: April 25, 2004, 22:26:10 Job time : 94 secs

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253 ThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsnGluIlePheLeuSerVal 272
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                                     754 ATATICIGITICIGITICITIACAATATCAATCTIAITITAIATTCTCTTGIGAGA
          LeuserHisGlnGluPhe---TrpAlaGlnLeuLysAsnLeuPhePheIleGlyValile
                                                                                                                                                                                                                                                                    APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30 MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REPERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMUNICATION INFORMATION:
TELECHONE: 202-371-2600
TELEPAX: 202-371-2600
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,948A CLASSIFTCATION: 435 RIOR APPLICATION: 435
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Matches:
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BULT, CAROL J.
SUTTON III, GRANGER G.
                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08467948A Patent No. 5998164
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CAO, LIANG
NI, JIAN
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TOPOLOGY: both
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USA
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NAME/KEY:
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Pred. No.:
Score:
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APPLICANT:
APPLICANT:
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352 AGCATTCTGTTCTAACCTGTATAGTGTAGATCGATTTTCTGGCAATTGTCTACCCATTT 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 ThrLeuvalilevalilevalvalProLeuvalValSerArgTyrGlylleHisGluGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 TIAACIĞITÜĞARĞBAĞBAĞIĞĞĞCĞĞCĞĞTITITIĞITÇAĞ ---TCTACCĞĞTÇIÇĞ 525
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172 ATCTGCGTCCTCAAAGTCCGAAATGAAACTACAACTTACATGATTAACTTGCCAATGTCA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 ThrPheLeuPheTyrValValileLeuValThrArgTyrLeu---IlePhePheLysCys 120
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen.
RAGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 9A-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION POR SEQ ID NO: 750:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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217.00
46.57%
27.08%
13.63%
FILING DATE: HEREWITH
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLONE: 417398
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Best Local Similarity:
Query Match:
                  CLASSIFICATION:
                                                                          FILING DATE:
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                      Sequence 1302, Application US/09016434

Patent No. 650038

GENERAL INFORMATION:

APPLICANT: Jaffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PALHARY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 314 PORTER DRIVE

STREET: GALIFORNIA

COUNTRY: USA
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY FAGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1302:
SEQUENCE CHARACTERISTICS:
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218.00
45.89%
22.78%
13.69%
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                                                                                                                                                                                                                                                                                                                                                                  HEREWITH
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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US-09-016-434-1302
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RESULT 13
US-09-016-434-1302
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                                                                                                                              97 IleHisMetTyrLeuThrPheLeuPheTyrValValIleLeuValThrArgTyrLeuIle
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14 GTCAACATGTTCACCCAGCATCTACTGTCTGACTGTGCTCAGCGTGGACCGCTACGTGGCC
                                                                                                                                                                                                                                                            117 PhePheLysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSer
                                                                                                                                                                                                                                                                                                                   574 GTGGTGCATCCCATCAAGGCGGCCCGCTACCGCCGGGCCCACCGTGGCCAAGGTAGTAAAC
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Sequence 750, Application US/09016434

Patent No. 650038

GENERAL INFORMATION:
APPLICANT: Jaffery J. Seilhamer
APPLICANT: Jeffery J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 AACTTCAAGGGTCTTTCCAAGGCATCCTATGCCTCAGGTGGAC 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 -----ValThrHisSerAsnAlaCysAsnSerLysValAlaPhe---
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ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PS-FECT 6.1 for Windows/MS-DOS 6.2
OPETWARE: --ANTION DATA:
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### Autorial Health	qq	ATGGTGGCCCTCAAGGCCGGCTGGCAGCACGCAAGACGCTCGGAGCGCAAGATCACC	US-10-0	
### A PARTICIAN PROPERTY OF SEASON PROPERTY OF SEAS	ò		ò	
### 1995/###################################	ପୁ	TTAATGGTGATGATGGTGATGGTGTTTTGTCATCTGCTGGATGCCTTTCTAC	සු	
Comparing   Comp	ò	ArgileTyrTyrLeuAsnVal	λö	==
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MATION:   Parametrica	nz-08-	417-103-1 ence 1, Application US/08417103	q <sub>Q</sub>	
### 141. Gramer 1.  Yamada, Yulichir C.  Selifor, Susumu  Selifor, Susumu  Selifor, Susumu  Oxintation  NULL Class 1.  Arnold, White & Durkee  D. Box 4433  Box 443  Box 4433  Box 4443  Box 4444  B	; Pate.		ò	
Selion Substitution   Substitution   Selion	æ æ 	Bell, Gr Yamada,	q	
### ADDRESS: 18  **NOR ADDRESS: 19  **NOR NUMBER: 10, Version #1.30  *	A FI	Seino, Su VENTION:	ò	
Armond, White & Durkee  P.O. Barnold, White & Durkee  B.O. Box 4433  United States of America  U	z ŭ		qq	
United States of America System: PC-Ocognatible Syst	- ;	E: Arnold, White P.O. Box 4433	λδ	
United States of America  United States of America  United States of America  Dabels Form  First Ploppy disk  SYSTEM: PC-Cox/Ms.Dox  Patentin Release #1.0, Version #1.30  LICATION DATA: US (08/417,103  ON NUMBER: US (08/417,103  ATION: 435  ON NUMBER: US (08/417,103  ATION: 435  ON NUMBER: US (08/417,103  ATION: 435  ON NUMBER: ARCD: 144  ATION: UNECRATION:  LOCATION DATA:  ON NUMBER: ARCD: 144  CATION UNIVER: ARCD: 144  CATION UN	·- ·-	ี่ อี อั	q	
PE: Floppy disk  IEM PC Compatible  SysTem: "PC-Dos/MS-DOS  PRESENTEN: PC-DOS/MS-DOS  PRESENTEN: PC-DOS/MS-DOS  PRESENTEN: PC-DOS/MS-DOS  PRESENTEN: PC-DOS/MS-DOS  PRESENTEN: PC-DOS/MS-DOS  PRESENTEN: PC-DOS/MS-DOS  DICATION DATA: "US/08/417,103  TE: 01-DEC-1991  TE: 01-DEC-199	•• ••	COUNTRY: United States of America ZIP: 77210	γò	
Section   Sect	· · ·	OMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	g	
Patentin Release #1.0, Version #1.30  LICATION DATA:  ON NUMBER: US/08/417,103  TE: 05-APR-1995  ATION: 435  CATION DATA:  ON NUMBER: US/08/417,103  TO: 01-DEC-1991  DN NUMBER: US 07/816,283  TO: 01-DEC-1991  DN NUMBER: US 07/816,283  TO: 01-DEC-1991  DN NUMBER: US 07/816,283  TO: 01-DEC-1991  DN NUMBER: ARCD: 144  CATION INFORMATION:  (512) 418-3000  CATION INFORMATION:  (512) 418-3000  CATION INFORMATICS:  (512) 428-3000  CATION INFORMATICS:  (512) 428-3000  CATION INFORMATICS:  (512) 428-3000  CATION INFORMATICS:  (512) 428-3000  CATION INFORMATICS:  DD 1024  CDS  CDS  CDS  CDS  CDS  CDS  CDS  CD			λō	
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ATION CATCAL STATES  ON NUMBER: US 07/816,283  ON NUMBER: US 07/816,283  ON NUMBER: US 07/816,283  ISON NUMBER: US 07/816,283  ISON NUMBER: US 07/816,283  ISON NUMBER: DD 0228  CATION INFORMATION: DD 910  (512) 418-3000  OR SEQ ID NO: 1: DD 910  OR SEQ ID NO: 1: DD 910  ISON SEQ ID NO: 1: DD 910  OR SEQ ID NO: 1: DD 910  OR SEQ ID NO: 1: DD 910  OR SEQ ID NO: 1: DD 910  ON 252  Illnear DD 1024  CDS  CDS  CDS  ID 1084		APPLICATION NUMBER: US/08/417,103 FILING DATE: 05-APR-1995	ò	
ON NUMBER: 10 07/816,283 ON NUMBER: 10 07/816,283 ON NUMBER: 21 28 1801, Mark B. 1801, Mark B. 1801, Mark B. 1801, Mark B. 1802, Mark B. 1801, Mark B. 1802, Mark B. 1803, Mark B. 1804,	Δ.	CLASSIFICATION: 435 RIOR APPLICATION DATA:	đ	
Best		APPLICATION NUMBER: US 07/816,283 FILING DATE: 01-DEC-1991	δ	
JON NUMBER: 3 / 1,228  JON NUMBER: 4 AKCD:144  CATION INFORMATION: (512) 418-2000	∢	NITHEN ALGENT INFORMATION:	qu	i
CALLON LINCEMALLON:  (512) 418-3000  (512) 474-7577  OR SEQ ID NO: 1:  ARACTERISTICS:  1624 base pairs  Cleic acid  Linear  CDS  CDS  CDS  CDS  CDS  CDS  CDS  CON  CDS  CDS  CDS  CON  CDS  CDS  CDS  CDS  CDS  CDS  CDS  CD		4 (	ð	228
12.1   44-75.7   12.1   44-75.7   12.2   44-75.7   12.2   45-75.7   12.2   45-75.7   12.2   45-75.7   12.2   45-75.7   12.2   45-75.7   12.2   45-75.7   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   12.2   1		TELECOMMONICATION: TELEPHONE: (512)	д	
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                                                                                                                                                 yHisAsnThrSerArgAsnSerSer --- CysAspProlleValThrProHisLeu
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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218.00
45.89%
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TOPOLOGY:
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                                                                                                                                                                                                                                                           137 AlaGlyMetTrpThrLeuVallleVallleValValProLeuValVal---SerArgTyr 155
                                                                                                                                                                                                                                                                                    681
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                   TATGTGATCCTGCGCTACGCCAAGATGAAGACC-----GCTACCAACATCTACATTCTA 381
SerileLeuPheLeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValile 56
                                                                                                   77 IleLysLysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHis 96
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                                                   AsnLeuValValValHisSerValPheLeuLeuThrValProPheArgLeuThrTyrLeu
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Patent No. 5436155
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVANTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Arnold, White & Durkee
STREET: PO Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Texas: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 ATCTCTTTCATCTACTCCGTGGTGTGCCTGGTGGGGGCTGTGTGGGAACTCTATGGTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 SerileLeuPheLeuLeuValLysMetAsnThrArgSerValThrThrMetAlaVallle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 AsnieuValValValHisSerValPheLeuleuThrValProPheArgleuThrTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AATCTGGCCATTGCTGATGAGCTGCTCATGCTCAGGTGCCCTTCCTAGTCACCTCCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 GTCAACÁTGTTCACCAGCATCTACTGTCTGACTGTGCTCAGCGTGGACCGCTACGTGGCC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911211
CLESSIFICATION: 435
ATTORNEY, AGENT INPORMATION:
NAME: MCDANIE, CS SEEVEN
TELECOMMUNICATION INFORMATION:
TELEPRAK: 713-789-2679
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Mismatches:
Indels:
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Matches:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: WUCLEIC ACID
STRANDEDNESS: double
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45.89%
22.78%
13.69%
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Best Local Similarity:
Query Match:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                      .63e-13
LENGTH: 1265 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                 218.00
45.89%
22.78%
13.69%
                                      , TOPOLOGY: linear
, MOLECULE TYPE: CDNA
US-07-816-283-3
                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                        Alignment Scores:
Pred. No.:
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                                                                               265 ---TyrasnGlullePheLeuSerValThrAlaIleSerCysTyrAsp
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                   Sequence 3, Application US/08417103
Facent No. 572239
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Samada, Yuichiro
APPLICANT: Samono, Susumu
ITLE OF INVENTION: Solution
ITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STARET: Texas States of America
COWNEY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-055-106C-2 (1-305) x US-08-417-103-3 (1-1265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
PILING DATE: 05-APR-1995
CLASSIFICATION: 435
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APPLICATION WINES: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARCD: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFRENCE/DOCKET NUMBER: ARCI
TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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218.00
45.89%
22.78%
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Best Local Similarity:
Query Match:
DB:
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, LOCATION:
US-08-417-103-3
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609 GCGGCCAACAGCGAC---GGCACGGTGGCTTGCAACATGCTCATGCCAGGCCCGGTCAA 665
                                                                                                                                                                                                             ThrTyr----ValLysIle1leAsnTyrMet1leValIle----PheValIleAlaValAla 193
                                                                                                                                                                                                                                                                                                                 726 GCTATCTGCCTGTGCTAC------GTGCTCATCATTGCTAAGATGCGC--- 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         819 GIGGIGCAGCIGGITAACGIGITIIGCIGAGGAGGACGACGACGCCACGGIGAGICAGCIGICG 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     939 GTCATCCTCGGCTATGCCAACAGCTGCGCAACCCCATCCTCTATGGCTTTCTCTCAGAC 998
::: ||| || ::: 489 GTGGTGCTGTTACCGCCGGCCACCGTGGCCAAGGTAGTAAAC 548
                                                                                                                               156 Gly1leHisGluGluTyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyr 175
                                                                             194 ValileLeuLeuValPheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHis
                                                                                                                                                                                                                                                                                                                                                                                                       768 ---ATGGTGGCCCTCAAGGCCGGCTGGCAGCGCAAGCGCTCGGAGCGCAAGGATCACC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,283
FILING DATE: 19911231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/07816283
Sequence 3, Application US/07816283
Setent No. 5456155
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATNOIG, White & Durkee
STREET: PO Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-789-2679
TELEFAX: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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72
73
121
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PILICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
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Matches:
Conservative:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMNICATION INFORMATION:
                                         ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas
                                                                                                        STATE: Texas
COUNTRY: United States of America
                                                                                                                                              ZIP: 77210
COMPUTER READABLE FORM:
MODIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (512) 418-3300
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1205 base pairs
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13.69%
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                             ORRESPONDENCE ADDRESS:
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15..1187
        NUMBER OF SEQUENCES:
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US-08-417-103-13
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                                                             6 ThrSerArgAsnSerSerCysAspProlleValThrProHisLeulleSerLeuTyrPhe 25
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                             US-10-055-106C-2 (1-305) x US-09-170-496D-35 (1-996)
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Patent No. 573299
Patent No. 573299
PAPLICANT: Bell, Graeme I.
APPLICANT: Yamada, Yuichiro
APPLICANT: Yamada, Yuichiro
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
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Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
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214 ATAATGACTTTACCCTTTCGAATGTTTTATTATGCAAAAGATGCATGGCCATTTGGAGAG 273
                             86 ProPheCysLysPheValSerAlaMetLeuHisIleHisMetTyrLeuThrPheLeuPhe 105
                                                                                             106 TyrValValileLeuValThrArgTyrLeuIlePhePheLysCysLysAspLysValGlu 125
                                                                                                                                                              126 PheTyrArgLysLeuHisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleVal 145
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Conservative:
Mismatches:
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US-09-170-496D-35
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; LIBRARY: GENBANK
; CLONE: g1066730
US-09-016-434-1064
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CLASSIFICATION:
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IMMEDIATE SOURCE:
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728 TCTGAGCAGAACGGCAGTGTCACATGATAGAGCTGAATCTCTATAAATTGCTAAG 787
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                                                                                                                                                        24 TyrPheileValLeuIleGlyGlyLeuValGly----ValIleSerileLeuPheLeuLeu
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                                                                  GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
TITLE OF INVENTION: PATHWAX GENE EXPRESSION
TITLE OF INVENTION: PATHWAX GENE EXPRESSION
UNDERS OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STRATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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Mismatches:
Indels:
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Matches:
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US-09-016-434-1064
; Sequence 1064, Application US/09016434
; Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1064:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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44.11%
22.90%
13.82%
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APPLICATION NUMBER:
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.-----TCCAGGTACATCCACAAATCCAGC 1029
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                                                                                                                                                                                                                                                                                                                                                                                    331 ACGCAGTCACCTATGTGAACAGCTGCTTGTTTGTTGCCCGTGCTGGTGATTCTGATCGGA 990
                                                                                                                                      LysCysLysAspLysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGly 138
                                                                                                                                                                          751 ÁAGCCATTTGGGGACTCTCGGATGTÁCAGCATAACCTTCACGAAGGTTTTAÍCTGTTTTTT 810
                                                                                                                                                                                                                                      159 GluGluTyrAsnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrVal 178
                               631 GGACCTTGGTACTTCAAGTTTATTCTCTGCAGATACACTTCAGTTTTGTTTTATGCAAAC 690
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                                                                                                                                                                                                              139 MetTrpThrLeuVallleValleValValProLeuValValSerArgTyrGlylleHis
79 LysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHis
                                                                   MetTyrLeuThrPheLeuPheTyrValValileLeuValThrArgTyrLeuIlePhePhe
                                                                                         APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Sllos-Santiago, Immaculada
ITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
ITLE OF INVENTION: 10se Thereof
FILE REPERENCE: 5800-88
CURRENT APPLICATION NUMBER: US/09/585,876
CURRENT PILING DATE: 2000-06-01
EARLIER APPLICATION DATE: 2000-06-01
EARLIER FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 IleGlyvalIleLeuValCysPheleuProTyrGlnPhePheArgIle---
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Patent No. 6586205
GENERAL INFORMATION:
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; LOCATION: (197)...(1237)
US-09-585-876-1
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ORGANISM: Homo sapiens
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1150 AGTCACTTAGACAGGCTTTTAGATGAATCTGCA-----CAAAAAATCCTATATTACTGC 1203
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|030 AGGCAATTCATAAGTCAGTCAAGCCGAAAAGCGAAAACATAACCAGAGCATCAGGGTTGTT 1089
                             --rccaecracarccacaarccaec 1029
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                                                                                                                                                                                                      247 TyrTyrLeuAsnValValThrHi8SerAsnAlaCysAsnSerLysValAlaPheTyr---
                                                                                                                               231 IleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIle------
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; OTHER INFORMATION: Incyte ID No. 6673545 1650519CB1
US-09-919-172-21
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Matches:
Conservative:
Mismatches:
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                                                                 219 GlnGluPheTrpAlaGlnLeuLysAsn------
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/09919172
Sequence 21, Application US/09919172
Sequence 21, Application US/09919172
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Thrner, Christopher M.
APPLICANT: PARSING CONCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 102
SEQ ID NO 21
LENGTH: 1444
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TGTTACATAGCCATA---
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43.13%
24.28%
14.51%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-09-919-172-21
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1058 TITAICAICCCITITGITAITAIAAITGICIGITACACAAIGAICAITITGACCITACIA 1117
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                                                                                                                                                            151 ValValSerArgTyrGlyIleHisGluGluTyrAgnGluGluHisCysPheLysPheHis 170
                                                                                                                                                                                                                                                                                                                                                                                       228 LeuphePhelleGlyVallleLeuValCysPheLeuProTyrGlnPhePheArgIleTyr 247
                                                   130
                                                                               880
                                                                                                       131 HisAlaValAlaAlaSerAlaGlyMetTrpThrLeuVallleVallalProLeu 150
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                                                                                                                                                                                                                 171 LysGlu---LeuAlaTyrThrTyrValLysIleIleAsnTyr-----MetIleValIle 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlullePheLeuSerValThrAlalleSer-----CysTyrAspLeuLeuPhe 283
IleHisMetTyrLeuThrPheLeuPheTyrValVallleLeuValThrArgTyrLeulle 116
                                                821 Triticcegiecartecaartertrecagrecagaacartaartregraaaa
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APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                   GICAACCICIAITGIAGCAICTICITIAIGACAGCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08988876
Patent No. 6063596
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MEDIUM TYPE: Diskett
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511 IGGATCTTCTTCCACATTAGGAATAAAACCAGCTTCATATTCTATCTCAAAAACATAGTG
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139
134
144
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Mismatches:
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Matches:
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                                                                                                              PF-0441
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGIGTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-04
TELEPHONE: 650-855-0555
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1444 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1650519
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43.13%
24.28%
14.51%
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TELEX:
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Best Local Similarity:
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                                                                                                               267 GluilePheLeuServalThrAlaileSer-----CysTyrAspLeuLeuLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 HisLeulleSerLeulyrPhelleValLeulleGlyGlyLeuValGlyVallleSerlle
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                                                                                                                                                                                                                                                                                                                   APPLICANT: SATHE, GANESH M.
APPLICANT: HILSEY, WENDY
APPLICANT: HILSEY, WENDY
APPLICANT: HILSEY, WENDY
APPLICANT: ELILS, CATHERINE E.
APPLICANT: FOLEY, JAMES J.
APPLICANT: SARAU, HENRY M.
APPLICANT: GHAMBERS, JON
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
FILE REFERENCE: GH-70001-1D1
CURRENT APPLICATION NUMBER: US/09/586,924
FRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FREIESE FOR Windows Version 3.0
SEG ID NO 1
SEG ID NO 1
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Mismatches:
Indels:
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Matches:
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48.06%
21.61%
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ORGANISM: HOMO SAPIENS
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Best Local Similarity:
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719 GTCAACCTCTATTGTAGCATCTTCTTTATGACAGCC---------ATGAGC 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 PhevalileAlaValAlaValIleLeuLeuValPheGlnValPheileIleMetLeuMet 207
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Mismatches:
Indels:
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Matches:
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      GH-70001-1
   REFERENCE/DOCKET NUMBER: GH-:
TELECHUNICATION INFORMATION:
TELEPAX: 610-270-5219
TELEPAX: 610-270-5090
TELEPAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                          2.76e-15
240.00
48.06$
21.61$
15.08$
                                                                                                                                                                     linear
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Best Local Similarity:
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MOLECULE TYPE:
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1479, Ap
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1021, Ap
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Sequence 1247, A
Sequence 1, Appl
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Sequence 4
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| Sequence | Application US/09044404A |
| Sequence | Application US/09044404A |
| Patent No. 6200775 |
| GENERAL INFORMATION: |
| APPLICANT: STITE, GANESH |
| APPLICANT: ELLIS, CATHERINE |
| APPLICANT: ARES, ROBERT |
| APPLICANT: SARAU, HENRY |
| TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR NUMBER OF SEQUENCES: ADDRESSE: SMITHKLINE Beecham Corporation STREET: 790 Swedeland Road, PORTION CITY: Kind of Potential Road, PORTION CITY: Kind of Potential Road, PORTION CITY: Kind of Potential Road, PORTION CITY: Rind of Potential Road, PORTION CITY: RING ROAD, PORTION CITY:
                                                                                                                                                                                                                     Sequence
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US-09-016-434-1302
US-09-016-434-1302
US-09-016-434-750
US-09-106-434-750
US-09-100-496D-11
US-09-100-496D-11
US-09-100-496D-11
US-09-106-434-1370
US-09-016-434-1370
US-09-016-434-1479
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US-09-016-434-1486
US-09-016-434-1190
US-09-016-434-1190
US-09-016-434-1190
US-08-7811-280-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IED COMPACIALO
COMPUTER: IED COMPACIALO
COMPUTER: IED COMPACIALO
COPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION NATE:
APPLICATION NUMBER: US/09/044,404A
FILING DATE: MARCH 19, 1998
CLASSIFTCATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: APRIC 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                              11143
111443
114493
11495
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-DBV TIMBOUT=120 -WARN TIMBOUT=30 -TRIREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPEXT=7
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1064, Ap
Sequence 35, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                          April 25, 2004, 20:06:25; Search time 87 Seconds (without alignments) 1945.517 Million cell updates/sec
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1592
1 MPGHNTSRNSSCDPIVTPHL......GGSHWFKQKIIGLMNCVLCR 305
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                    - nucleic search, using frame_plus_p2n model
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US-08-988-876-4
US-09-919-172-21
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US-07-816-283-1
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Maximum Match 100%
Listing first 45 summaries
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Xgapp 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2646964642

Result

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Unpublished (2002)
Contact: Koop BF
Contact: Koop BF
Contact: Koop BF
Contact: Koop BF
Contact: Coop BF
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Biagi, Mitch Uh and Robert Devlin (DPO, Vancouver, B.C.),
Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery
(Crofton, B.C.), Rachel Roper (University of Victoria)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 HisGlnGluPheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCys 237
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                                   http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
GRASP Consortium, Davidson, W.S., Koop, B.F. and
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Matches:
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Search completed: April 25, 2004, 22:16:30 Job time : 2909 secs

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Actinopterygii, Neopterygii, Teleostei; Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Salmo.

    (Dases 1 to 733)

                                                                                                                                                                                                                                                                                                                                                                                                                                   251 ValvalThrHisSerAsnAlaCysAsnSerLysValAlaPheTyrAsnGlullePheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 SerValThrAlaIleSerCysTyrAspLeuLeuLeuPheValPheGlyGlySerHisTrp
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A survey of Salmo salar transcripts from high complexity cDNA
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CASS0323
CASS0323.1 GI:24380566
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Genome Sciences Centre, BC Cancer Agency
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Centre for Biomedical Research
University of Victoria
Do Box 3200 STN CSC, Victoria BC,
Tel: 250 472 4067
Fax: 250 472 4075
                     /db_xref="taxon:10090"
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mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                       6.35e-23
305.00
86.49%
75.68%
                                               sex="male"
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Unpublished (2002)
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SOURCE
ORGANISM
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CA050323/c
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Pred. No.:
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AUTHORS
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A linear EST 16-MAY-2003 CDNA, mRNA sequence.
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                                                                                                                                      /organism="salmo salar"
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Genetics; Atlantic salmon tissue contributors: Carlo
Bagi, Mitch Uh and Robert Devlin (DFO, Vancower, B.C.),
Simon Jones (BSS, Nanaimo, B.C.), Seaspring Hatchery
(Crofton, B.C.), Rachel Roper (University of Victoria)"
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 648)
cDNA preparation, sequencing and bioinformatics:
Y Butterfield, R Kirkpatrick, J Asano, N Girn, R Guin, D Lee,
S Lee, T Olson, P Pandoh, A Prahbu, D Smailus, L Spence, J Stott,
S Taylor, G Yang, J Schein, S Jones and M Marra.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 PheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyVallleLeuValCysPheLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 LysValAlaPheTyrAsnGluIlePheLeuSerValThrAlaIleSerCysTyrAspLeu
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288.50
59.03%
39.58%
18.12%
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307 TGCTATATGTGT 296
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EST 01-FEB-2001
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Mus musculus
Eukaryotailus
Eukaryotai Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I. (bases 1 to 478)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 IleSerLeuTyrPheIleValLeuIleGlyGlyLeuValGlyValIleSerIleLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Met Proglyki gagn Thr Serargagn Ser Ser Cysasp Prolleval Thr Prohisteu
                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol Lype="mRNA"
/db Zref="taxon:9606"
/tiseue type="normal nasopharynx"
/clone lib="human nasopharynx"
/nore="ESTS generated from a normal nasopharynx"
library from southern Chinese"
Transcriptional Gene Expression Profile of Human Nasopharynx Unpublished (2003)

Contact: YiXin Zeng
Cancact: YiXin Zeng
Cancac Center
Cancac Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG145683 478 bp mRNA linear ES
mac33c07.y1 Soares mouse 3NbMS Mus musculus cDNA clone
IMAGE:4001652 5', mRNA sequence.
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Mismatches:
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Location/Qualifiers
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Seq primer: -40RP from Gibco
High quality sequence stop: 3
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ESTI6303 human nasopharynx Homo sapiens cDNA, mRNA sequence.
CD699779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuPhePhelleGlyValIleLeuValCysPheLeuProTyrGlnPhePheArgIleTyr 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 TGCTTCTTCCTTCTAGTAATAGTCGTCTGTTTTATACCCCACCATGCATTCCGGGTACAC 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 LysPheHisLysGluLeuAlaTyrThrTyrValLysIleIleAsnTyrMetIleVallle 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 PhevalileAlavalAlavalIleLeuLeuValPheGlnValPheIleIleMetLeuMet 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 ValGlnLysLeuArgHisSerLeuLeuSerHisGlnGluPheTrpAlaGlnLeuLysAsn 227
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        polyA+ RNA from equine peripheral blood leukocytes isolated from a healthy adult horse. The leukocytes were stimulated for 4 hr with 10 ng/ml E. coli 05:85 LDS. Double-stranded cDNA was cloned unidirectionally into different Drail sites of the pMERBS-FL3 vector (5-prime DrailI site is CACTOTOGT, 3-prime DrailI site is CACTOTOGT, 3-prime DrailI site is CACCATGTO.
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 499)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
                                                                                                                                                                                                                                                                                                                                                                                             2 ATTGTCATATTCCGATTGCTCATCTATTTAAG---AAACTCCAACTGCAACAGTTAAAA 58
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Equus caballus

Equus caballus

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bummalia, Entheria, Perissodactyla, Equidae, Equus.

I (bases 1 to 679)

Ss Vandenplas,M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S.,

An Osre,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.

An EST database from equine (Equus caballus) stimulated peripheral

blood leukocytes

An EST database from equine (Equus caballus) stimulated peripheral

blood leukocytes

Contact: Cordonnier-Pratt MM

The University of Georgia, Department of Plant Biology

Plant Science Building, Rm. 2502, Athens, GA 30602-7271, USA

Fax: 706 542 1860

Fax: 706 542 1860

Fax: 706 542 1860

Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo Institute of Medical

Science: tissue and RNA were prepared in the Department of Large

Animal Medicine, University of Georgia, sequenced as presented as their

reverse complement and have been trimmed to exclude vector and regions below

Phred quality 16. Three-prime sequences are presented as their

reverse complement and have been trimmed to exclude polyA.

Seq primer: Sugs (CTTCTGCTCTAAAAGCTGCG).
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LeukoS2_2 H07.gl_A024 Stimulated peripheral blood leukocytes S2
Equus caballus cDNA clone LeukoS2_2_H07_A024 5', mRNA sequence.
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/lab host="DHIOB-T1 phage-resistant E. coli"
/lab lib="Stimulated peripheral blood leukocytes S2"
/note="Organ: circulatory system; Vector: pWB185-FL3;
Site_1: Xho1; Site_2: Xho1; The library was prepared from
                                                                                                            267
                                                                                                                                                                                                                                                                                                                          314
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                                                                    60 lvalHisSerValPheLeuLeuThrVal-ProPheArgleuThrTyrLeuIleLysLysT
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/clone="LeukoS2_2_H07_A024"

    .679
    /organism="Equus caballus"
/mol_type="mRNA"
/strain="thoroughbred"

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1 (bases I to 649)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Mhitington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mysk, R., Smith, E., Veloso, M., Klika, A., Hess, J., Cothren, K., Lo, K., Creation of genome-wide protein expression libraries using random activation of gene expression

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/mol type="mRNA"
/db xref="taxon:9606"
/doll inne="HTNA"
/db xref="taxon:9606"
/coll line="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
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                                                                                                                                                                                                                         LysLeuHisAlaValAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValVal 148
                                                                                                                                                                                                                                                                                              122 Argecrégécacadaracr------criar-ceraragréacacecaerra 165
                      IleleuvalThrargTyrLeuIlePhePheLysCysLysAspLysValGluPheTyrArg 128
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RST44080 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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Mismatches:
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Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG461295.1 GI:13749801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.67e-28
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                                  109
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ORGANISM
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CA355790 680 bp mRNA linear EST 05-NOV-2002 627748 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT88K09_A_F05 5',
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1. (base 1 to 680)

Rexroad, C.E. and Keele, J.W.

Sequence analysis of a rainbow trout normalized cDNA library
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                     Contact: Rexroad CE
USDA, ARS. National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroaddencicra ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.
Seq primer: AGGGGATAAATTTCACAGGAA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clome_lib="NCCCWA 1RT"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from brain, gill, liver:
spleen, muscle, and kidney."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 GTCAITGGGGTCAICGGG---ITGGCCCTGAIGAICCACATCCAATCCAACAIGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AsnSerSerCysAspProlleValThrProHisLeulleSerLeuTyrPheIleValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 IleGlyGlyLeuValGlyValIleSerIleLeuPheLeuLeuValLysMetAsnThrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 ValProPheArgLeuThrTyrLeuIleLysLysThrTrpMetPheGlyLeuProPheCys
739 ATGGAAGGACANGGTAGAGTTTTATAGAAAGCTNCATGCCATTGCT 784
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337
34
44
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/organism="Oncorhynchus mykiss"
/nol type="mkNA"
/db_xref="taxon:8022"
/clone="IRRB8K09 A_F05"
/tissue_type="pooled"
/lab_hose_"DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                  Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
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Pred. No.:
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KEYWORDS
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                                                                                   DEFINITION
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AUTHORS
TITLE
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COMMENT
                                  RESULT 9
CA355790
                                                                                                                     ACCESSION
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AJ455645
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                   sGlnGluPheTrpAlaGlnLeuLysAsnLeuPhePheIleGlyValIleLeuValCysPh 238
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                                                                                                                                                                                                                                               Gallus gallus (chicken)
Gallus gallus
Gallus galus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 834)
Euerstedde, J. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 2, 20251 Hamburg, Germany
Email: WEL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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/dev_stage="2-3 weeks old"
/clone_llb="riken!"
/noce="CB inbred strain"
                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="6b4r1"
                                                                                      238 eLeuProTyrGlnPhePheArglleTyr 247
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Best Local Similarity:
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CA965628
ECA965628.1 GI:27492185
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Site_2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lochar Hennighausen/Priscilla Purth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
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Cyprinus carpio acrpio
Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
1 (bases 1 to 844)
Gracey, A.Y., Fraser, E., Li, W. and Cossins, A.R.
Microarray and EST analysis of the carp (Cyprinus carpio)
Microarray and Cossins of the carp (Cyprinus carpio)
Microarray and Cossins analysis of the carp (Cyprinus carpio)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Enological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 72B
Tel: +44(0)151-795-44510
Fax: +44(0)151-795-4431
                                                                                                                                                                                                                                                                                                                                                                                                     367 ACATCGATTTACTTCATAGTGCTCATTGGAGGACTGGTAGGCCTCATCTCCATCCGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                            41 LeuLeuValLysMetAsnThrArgSerValThrThrMetAlaVallleAsnLeuValVal
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Conservative:
Mismatches:
Indels:
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clone="IMAGE:4917024"
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494.00
90.27%
85.84%
31.03%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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Site_2: Sfil GGCGCTGGCC; Normalized and serially subtracted oDNA library prepared from mixed tissues of warm, cold and hypoxia challenged animals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||||||:: :::::: :::: TITCCAAGTTTATTTGAAAGGCCACATGTCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eLysCysLysAsplysValGluPheTyrArgLysLeuHisAlaValAlaAlaSerAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 yMetTrpThrLeuVallleVallleValValProLeuValValSerArgTyrGlyIleHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 BGluGluTyrABnGluGluHisCysPheLysPheHisLysGluLeuAlaTyrThrTyrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           llysilelleAsnTyrMetileValilePheValileAlaValAlaValIleLeuLeuVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 ACAGAAC---GATTCAACTCATTGCTTTAATTTTTGGTCAGGCTCTCACCCCAGCCTACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1PheGlnValPheIleIleMetLeuMetValGlnLysLeuArgHisSerLeuLeuSerHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 ValvalHisSerVal-PheLeuIhrValProPheArgLeuThrTyrLeuIle---Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 slysThrTrpMetPheGlyLeuProPheCysLysPheValSerAlaMetLeuHisIleHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheLeuLeuValLysMetAsnThrArgSerValThrThrMetAlaValIleAsnLeuVal
Vector has been trimmed from this EST.

Plate: 15 row: h column: 17
Seq primer: TriplEx 5' LD (5'-CTCGGGAAGCGCGCCATTGTGTTGGT-3')

High quality sequence start: 39

High quality sequence stop: 580.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
92
74
74
84
3
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Mismatches:
Indels:
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Matches:
                                                                                                                             1. .844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-844)
                                                                                                                                                                                                                           /sex="Male & female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-055-106C-2 (1-305) x CA965628
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646 bp mRNA linear EST 29-MAY-2001
602796201F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917024 5',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerValThrAlaileSerCysTyrAspLeuLeuLeuPheValPheGlyGlySerHis--- 289
                                                                                                                                                                                                                                                                                                                                               LysGluLeuAlaTyrThrTyrValLysIleIleAsnTyrMetileValIlePheValIle 190
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 646)
1 Marinae http://mgc.nci.nth.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1097 AATTITCCAGAGCAAGAA-----AATICTAAGTIAATICTGTACAATGAAATCTGTGTT
   680 CTTCGGCTCATCTATTTAAG---AAACTGCAAATGCAACAGTTACAAAGTTCCAT
                                                                                                                                                                                                                                                               917 ACAACAGTICTGCTCTTTCTGATACAGATGGCTGTCATTCTTTTTGATAAAAGCC
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Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
                                                                                                   132 AlavalAlaAlaSerAlaGlyMetTrpThrLeuValIleValIleValValProLeuVal
                                                                                                                                                        GCCGTGGCTCTAAGTATTATTTGGGTGACGAAGCTTCATCTTTTACCAATATTT
                                                                                                                                                                                                                       152 ValSerArgTyrGlyIleHisGluGluTyrAsnGlu---GluHisCysPheLysPheHis
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0828 row column: 01
High quality sequence stop: 644.
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Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mall:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-922, Pax:81.45-503-9216)

Pax:81.45-503-9216)

Pax:81.45-503-9216)

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues: plane for further details.

URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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440 ACCGTIGGAACAGTIAIGAIGICACACACAIGAIGTIT 499
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/mol type="mRN"
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 61
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo. [hoses 1 to 456] [hoses 1 to 456] [hoses 1 to Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Mahairas, G.G., Wallace, J.C., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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Craniata, Vertebrata, Buteleostomi;
Catarrhini, Hominidae, Homo.
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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|mol type="genomic DNA"
|db xref="taxon:9606"
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of 60,700 full-length cDNAs

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, T., Hirozane, T., Katoh, H., Kayawi, T., Kayawi, T., Kayawi, T., Kayawi, T., Katoh, H., Kayawi, T., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakai, K.,
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                     267 GluilePheLeuSerValTh@RlaileSerCysTyrAspLeuLeuLeu
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ligh-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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S Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Xrol, M., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999) other Gsequences from Library RPCI-23

Contact: Shaying Zhao

Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
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                                                                                                                                                                         | HishlavalalaAlaSerAlaGlyMetTrpThrLeuvallleVallleValvalProLeu 150
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                                                                                                                                                                                                                                                         360 GTGGTTTCTCAGTATGGAAATAGGAAGAATACAATGAGCAACAGTGCTTTAGATTCCAT 419
                                                                                                                                                                                                                                                                                                   171 LysglubeualaryrThrTyrValLyslleileAsnTyrMetileValilePheVallle 190
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HS_3162_B1_B01_MR_CIT_Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3162 Col=1 Row=D, genomic survey
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Matches:
Conservative:
Mismatches:
Indels:
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 772)

8 NIH-MoG http://mgc.nci.nih.gov/.

1 (bases 1 to 772)

8 NIH-Mod http://mage.lln.nih.gov/.

8 Consortium (LLNL)

8 DNA Sequencing by: Incyte Genomics, Inc.

8 Consortium/LLNL at:

8 Http://mage.lln.gov/

8 Plate: LLAM9196 row: f column: 07

8 High quality sequence stop: 634.

8 Location/Qualifiers

8 Location/Qualifiers

8 Lice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                       BF160725
601769127F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988230 5', mRNA sequence.
BF160725
BF160725.1 GI:11040832
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                                   430 AAGGITGCATITIAIAACGAAATCTTCTTGAGTGTAACAGCAATTAGCTGCTATGATTTG
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88.02%
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                                                                                                   Lotoste, L. C. Coord, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Mattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submitseion

Birect Submitseion

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-065C);
Tel:81-45-503-9111, Pax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC clone are derived during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Male BAC Library"
     Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         684
0 0
6 0
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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/molltype="genomic DNA"
/db xref="taxon:9598"
/clone="RP43-007G22.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-055-106C-2 (1-305) x AG145972 (1-684)
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Vector : pBACe3.6
R.Site 1 : ECORI
R.Site 2 : ECORI.
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938.00
96.76%
96.76%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                         PRIMERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                       TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                   TITLE
JOURNAL
                     AUTHORS
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AG145972 684 bp DNA linear GSS 08-JAN-2002
Pan troglodytes DNA, clone: RP43-007G22.TJ, genomic survey
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                              BG862323
CA65628
AJ455645
CA55790
BG461295
CD69927
CD699779
BG195633
CA650323
CB514250
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AG145972.1 GI:16675650
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29: gb_gss2:*
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214.5
211.5
210.5
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538.5
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AG145972
                                                                                                                                                                                                                                                                                                                 Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
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-Q=/cgn2_1/USPTO_spool/US10055106/runat_2104204_161131_26191/app_query.fasta_1.455
-DB=EST -CPMT=fastap -SUPFTX=p2n.rest -MINMATCH=0.1 -LOOPEX=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blooum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXEN=200000000
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-USER=US10055106_GCGS1 1_LE 2810_GCN=12 -DSPENGCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                             (without alignments)
3136.352 Million cell updates/sec
                                                                                                                                                                                               US-10-055-106C-2
1592
1 MPGHNTSRNSSCDPIVTFHL......GGSHWFKQKIIGLWNCVLCR 305
                                                                                                                           April 25, 2004, 19:56:50 ; Search time 2904 Seconds
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                           OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                         27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                     0.5
7.0
7.0
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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AX406931 MNS muscu
AX406929 Homo sapi
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AX406929 Homo sapi
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